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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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11597.602 Million cell updates/sec
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ALIGNMENTS

RESULT 1

AR086858		
DEFINITION	Sequence 1 from patent US 5985634.	
ACCESSION	•	
VERSION	AR086858.1 GI:10013624	
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE		
AUTHORS	Schmidt, R.R. and Miller, P.	
TITLE	the .alpha	
	.betasubunits of glutamate denydrogenases and methods of use	
JOURNAL	Patent: US 5985634-A 1 16-NOV-1999;	
ecano cano man	1. 2140	
	/organism="unknown"	
ORIGIN		
~	100.0%; Score 2140;	
Matches 2140;	les 2140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Ş	1 CTCCTTTCTGCTCGCCCTCTCTCCGTCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTA 60	
Db	1 CTCCTTTCTGCTCGCCCTCTCTCCGTCCCGCCATGCAGACCGCCTCGTCGCCAAGCCTA 60	
Qγ	61 TCGTGGCCGCCCGGCTGGCGCACGCCCGCGCGCGCGCGCG	
Db	61 TCGTGGCCGCCCGCTGGCGCGCACGCCCGCGCCGCGCGCG	
γQ	121 TCCGCTCCGCCAAGCGCGATGTCCGCGCCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCG 180	
ם	121 TCCGCTCCGCCAAGCGCGATGTCCGCGCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCG 180	
φ	181 CGATGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA 240	
Db 1	181 CGATGGACGCCACCACCACGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA 240	
Qy	241 CCAAGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGGACGTGCGCCAGCTGC 300	

1081 GCTTCACGCGGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAACAACAGCGCCC 1140	241 CCAAGGCGGGCACTCAGGGCCTCGTTCCACGGCCTCAAAAACCCCCACCGGCTGCGGCCACCTCGTTCCAGGCCACTCAAAACCCCCACCGGCTGCGGCCAGCTCCAGGCGGGGGCAGCTCAAGGCCCGGGCAGGCGGGGGGGG
RESULT 2 AR086871 LOCUS DEFINITION Sequence 18 from patent US 5985634. ACCESSION AR086871 VERSION AR086871.1 GI:10013637 KEYWORDS SOURCE ORGANISM Unknown. Unknown. Unknown. FOLYpeptides and Miller, P. FOLYpeptides and polymucleotides relating to the .alpha and .betasubunits of glutamate dehydrogenases and methods of use JOURNAL FEATURES SOURCE JOURNAL Patent: US 5985634-A 18 16-NOV-1999; Location/Qualifiers 12137 /organism="unknown"	Db 1321 CCTCACCAACGAGGCCATCCACAACGACCAACGACGCCTGCAACTACTCTACTCTCCCCGGCA 1380 1381 AGGCGGCAACGCCGGCCGCTGGCGGTCAGCGGCCTGAAGATGACCCAGAACCGGATCAT 1441 GCCTGAACTGGACTGCCAGGGGTTCGGGAAAGCTGAACCCAGAACCGAACCGATCAT 1441 GCCTGAACTGGACTGCGAGAGGTTCGGGAAAAGCTGAACCGAACCCAGAACCGATCAT 1441 GCCTGAACTGGCACGGGGCGTTCGCGAAAGCTGAACCGAACCTACAGGACCATCAT 1441 GCCTGAACTGGCACGGGGCGTTCGCGAAAGCTGAAAGCTGAACCGATCATCAAAGGACATCT 1501 ACGACTCCGCCATGGGGCCGTTCCGCGAAAGCTTGAAAGCTGAAACCTGATCATCAAAGGACATCT 1501 ACGACTCCGCCATGGGGCCGTTCCCGAAGACTTCAACGGCCAACCTACCT

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964 GCTGCCTGGTGTCTGGCGCGGGCAACGTGGCCCAGTACTGCGCGGGAGCTGCTGCTGGAGA 1023	904 GCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGACAAGGGCGAGAGCCTCAAGGGCAAGC 963 	844 TGACCCCGAAGGGCCAGGAGTATGGCGGCCTCCGAGATCCGCCCGAGGCCACCGGCTACG 903	784 GCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGGATCACCAAGAACTACACCGGCGTGC 843.	724 TGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGCCGGCGACATCGGCGTGGGCGCGC 783	664 ACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCGAGC 723	604 TCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGAAGGGGCGGCTCCGACTTCG 663	544 GCTGCGCTTCCACCCCTCCGTGAACCTGTCCATGAAGTTCCTTGCCTTTGAGCAGA 603	484 TGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAAGGGCG 543	424 TCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTTCCTGGACGGCGACGCCGGCAACC 483	364 CCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGCAGA 423	304 CCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTGG 363	244 AGGCGGGCACTGAGGGCCTCGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGCTGA 303	184 TGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCACCA 243	124 GCTCCGCCAAGCGCGATGTCCGCGCCAAGGCCGTCTCGCTCG	64 TGGCCGCCCGCTGGCGGCACGCCCCGCGCTGCGCCGTGGCCGTGGGCTGCGCGTGGGTCC 123	4 CTTTCTGCTCGCCCTCTCCGGTCGCGCCATGCAGACCGCCCTCGTCGCCAAGCCTATCG 63	Query Match 99.9%; Score 2137; DB 6; Length 2137; Best Local Similarity 100.0%; Pred. No. 3.4e-242; Matches 2137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/mol_type="unassigned DNA" .
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Db 499 GCGGCCTGCCGCGACCCCCTGCCCATGGGCGGCAAGGGCGGCTCCGACT 660 Qy 601 AGATCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGAAGGGCGGCTCCGACT 660	481 ACCTGCAGGTCAACCGCGGGCTTCCGCGTGCAGTACTCGTCCGCCCATCGGCCCTACAAGG 5	QY 421 AGATCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGACGACGACGCCGGGA 480	361 TGGCCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGC	Qy 301 TGACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGG 360	241 CCAAGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGC	OY 181 CGATGGACGCCACCGGCGGCGTGCACAGAAGGCGGTGAAGCAGATGGCCA 240	Qy 121 TCCGCTCCGCCAAGCGCGATGTCCGCCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCG 180	61 TCGTGGCCGCCCGCTGGCGGCACGCCCGCGCTCGCGCCGTGGCCGTGCGCGTGGG	GCAGACCGCCCTCGTC GCAGACCGCCCTCGTC	Query Match 95.6%; Score 2046; DB 6; Length 2099; Best Local Similarity 98.0%; Pred. No. 1.7e-231; Matches 2098; Conservative 0; Mismatches 0; Indels 42; Gaps 1;	rce	Polypeptides and polynuc betasubunits of gluta .betasubunits of gluta Patent: US 5985634-A 3 1	ORGANISM Unknown. ORGANISM Unclassified. Unclassified. REFERENCE 1 to 2099) NUTUONS CONTACT D 2004 Millor D	ION AR086859.1 GI:10013625 DS	AR086859	2101 AACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAAAAAA	OV 2104 PACACGACGACTCAAAAAAAAAAAAAAAAAAAAAAAAAAA
Db 1579 AGGCCCAAGCCACCGGCTCACCGGCAACCAACCAACCAAC	1621 AGGCCCAAGGCTCACCGGCAATCCAACCCAACCAACCTAAGGCCAGGACCTTTT 1	Dy 1501 ACGACTECGCCATGGGGCCGTCCGCAGATACAATGTIGACCTGGCTGTTTAAGCTGCCC 1620 1459 ACGACTECGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGTTTTAAGCTGCCCACA 1518 OV 1561 TCGCGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGGGCGCTGTTTAAGCTGCCC 1620	1441 GCCTGAACTGGACTCGGGAGGAGGTTCGCGAACAGCTGGAGGGCATCATGAAGGACATCT 15	13 14	1321 CCTCCACCAACGAGGCCATCCACAAGTACAACGAGGCCGGCATCATCTACTGCCCCGGCA	Oy 1261 ACGACGCCGAGCTGCTCATCAAGCACGGCTGCCAGTACGTGGTGGAGGGCGCCAACATGC 1320	1159 AGCTGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATGAGC	1141 1099 1201		1 AGAAGGGCGCCATCGTGCTGTCGCTGTCCCACTCCCAGGGCTACCGTGTACGAGCCCAACCG	Qy 961 AGCGCTGCCTGGTGTCTGGCGCGGGCAACGTGGCCCAGTACTGCGCGGAGCTGCTGCTGC 1020	Oy 901 ACGGCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGACAAGGGCGAGAGACCTCAAGGGCA 960	Qy 841 TGCTGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGCT 900	Qy 781 CGCGCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCCAAGAACTACACCGGCG 840	Qy 721 AGCTGCAGGGCCACATCAGCTACGTGCAGGACGTGCCGGCGGCGACATCGGCGTGGGCG 780	Qy 661 TCGACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCG 720	Db 559 AGATCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGAGGGCGGCTCCGACT 618

Db 61 TGGCC	Query Match 95.5%; Score 2043; DB 6; Length 2096; Best Local Similarity 98.0%; Pred. No. 3.8e-231; Matches 2095; Conservative 0; Mismatches 0; Indels 42; Gaps Oy 4 CTITCTGCTCGCCCTCTCCCGTCCCGCCATGCAGACCCTATCG 63	REFERENCE 1 (bases 1 to 2096) AUTHORS Schmidt, R. R. and Miller, P. TITLE Polypeptides and polynucleotides relating to the .alpha and .betasubunits of glutamate dehydrogenases and methods of use JOURNAL Patent: US 5985634-A 19 16-NOV-1999; FEATURES Location/Qualifiers source /organisms="unknown" ORIGIN			Qy 1741 GCCGCCGTGCCATTCCACCCCAAGAAGAACTAGCGGCACTTGACTGCATCAGGA 1
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MADP-gdh gene; NADP-specific glutamate dehydrogenase.

Chlorella sorokiniana

Chlorella sorokiniana

Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae;

Chlorellales; Chlorellaceae; Chlorella.
                               Cock, J.M., Kim, K.D., Miller, P.W., Hutson, R.G. and Schmidt, R.R. A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP-specific glutamate dehydrogenase(s) in Chloroplastic NADP-specific glutamate dehydrogenase(s)
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Schmidt, R.R.
Direct Submission
Submitted (03-APR-1991) R.R. Schmidt, U
of Microbiology and Cell Biology, 3103
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Query Best L Matche	SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE ORIGIN	RESULT 6 AR086860 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	g 4g	ם מם	& B	8	B 8	g Qy	p Q	Qy Db	D Qy	B 8	B &	₽ \$	\$ B \$
y Match 92.0%; Score 1969; DB 6; Length 1969; Local Similarity 100.0%; Pred. No. 1.9e-222; hes 1969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Unknown. SM Unknown. Unclassified. E 1 (bases 1 to 1969) S Schmidt, R.R. and Miller, P. Polypeptides and polynucleotides relating to the .alpha and Polypeptides of glutamate dehydrogenases and methods of use .betasubunits of glutamate dehydrogenases and methods of use Location/Qualifiers Location/Qualifiers 1. 1969 /organism="unknown" /mol_type="unassigned DNA"		2133 AAAAAAAA 2140 2092 AAAAAAAA 2099	032 TGCGATACTGTGACCTGAGAGTGCTTGTGTAAACACGACGAGTCAAAAAAAA	TAGCCTGGTGACCCCAAGTAGCAGTTAGTGTAAACACGACGAGTCAAAAAAAA	Ö	1953 CTTTTAGTGTATGTGCGCCCCCTCCTGCCCCGAATTTTCCTGCCATGAGACGTGCGGTT 2012	1893 GCTCGGTTTTGACCCCCTCCAGTCTACCCACCCTGTTGTGAAGCCTACCAGCTCAATTGC 1952	1833 GAGAGCCTCTCTCCCCCGAGCCCTAAGCGCTGACGTCCGCCCGACTTTGCCTCGCACATC 1892	1773 GAACTAGCGGCACTTGACTGCATCAGGACGGCTATTTTTTTCGCGACGCGCGCTCACCCC 1832	1713 TCACCTGCCCTTTCATAACCCTGCTATTGCCGCCGTGCCCCTGCAATTCCACCCCAAGAA 1772	1653 CCAACCAACTCAACGGCCAGGACCTTTTCGGAAGCGGCGCCTTTTTCCCAGCCAG	1593 AAGGCCCAGGGCCTGTTTAAGCTGCCCAGGCCCAAGCCACGGTCACCGCCAATCCAAC 1652	1533 ARTISTICANCINGCINGUEGECCAACATICGCUGECTICACCAAGGTGGCTGATIGCCGTC 1592	.473 AAGCTGGAGCGCATCATGAAGGACATCTACGACTCCGCCATGGGGCCGTCCCGCCAGATAC 153

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AUTHORS 1 (bases 1 to 1506) Schmidt, R.R. and Miller, P.

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1506 bp patent US 5985634.

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                                                                                         GACGTGCCCGCCGGCGACATCGGCGTGGGCGCGCGCGAGATTGGCTACCTTTTCGGCCAG
                                                                                                                                                      GTGATGCGCTTCTGCCAGTCCTTCATGACCGAGCTGCAGCGCCACATCAGCTACGTGCAG
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        GTGGCCCAGTACTGCGCGGAGCTGCTGGTGGAGAAGGGCGCCATCGTGCTGTCGCTGTCC
                             CTGAAGGACAAGGGCGAGAGCCTCAAGGGCAAGCGCTGCTGGTGTCTGGCGCGGGCAAC
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GTGGCCCAGTACTGCGCGGAGCTGCTGCTGGAGAAGGGCGCCATCGTGCTGTCGCTGTCC
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                                                                                                                                   Unclassified.

1 (bases 1 to 1473)
Schmidt,R.R. and Miller,P.
Schmidt,R.R. and Miller,P.
Polypeptides and polynucleotides relating to
beta.-subunits of glutamate dehydrogenases
Patent: US 5985634-A 25 16-NOV-1999;
Location/Qualifiers
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GCCGAGCTGCTGATCAAG(GACTGCCAGGTGGA GACTGCCAGGTGGA	CGAGTACAAG CGAGTACAAG	CGCGAGCA(GGCGCCATCGTGCT GGGCCATCGTGCT	;CTGCCTGGTGTCTGGCG; CTGCCTGGTGTCTGGCG;	GCCGTGCTGTTTGTGGAGAAC	CCCCGAAGGG CCCCGAAGGG	GAGATTGGCTACC agattggctacc	CAGCGCCACATCAG CAGCGCCACATCAG	CCCAAGGGCAAGAG(CTTCAAGAACAGCCT	GCCTGCGCTTCCACC	CAGGTCAACCGCGG CAGGTCAACCGCGG	GTTGAGCCTGAGCG	GTCTCCCTGCAGC	CGAGATCTTCATGAA 	GCGGGCACTGAGGG CGGGCACTGAGGG
PACGGCTGC PACGGCTGC	CATCGCCTTCCC CATCGCCTTCCC	AGCGACACCGCCGTGT	3CTGCAGGCGGTGCAGG	GTCGCTGT	;cgcgggcaacgtggccc 	g=g	CAGGAGTATGGCGGC	CTTTTCGGCCAGTAC	CTACGTGCAGGAC)CGACGCGGAGGTGATGC 	GACCACCCTGCC GACCACCCTGCC	CCCTCCGTGAACCTG	CTTCCGCGT	CGTGATCACCTTC CGTGATCACCTTC	CCCGTGTTCGAGAAG CCCGTGTTCGAGAAG	GGACCCGGAGCAC GGACCCGGAGCAC	CCTGGTGCACGG CCTGGTGCACGG
CAGTACGTGGTGG CAGTACGTGGTGG	CTGCGCCACCCAGAA	FTATGTGGGCGACCG	GACATGAAGAAGAAGAACAAC 	CCGACTCCCAGGGCTACG: CGACTCCCAGGGCTACG:	AGTACTGCC	GCTGAAGGACAAGGGCGJ 	TCCGAGATCCGCCC	AAGCGCATCACCAA AAGCGCATCACCAA	GTGCCCGCCGGCGA	ATGCGCTTCTGCCA ATGCGCTTCTGCCA	CATGGGCGGCGAA 	CCTGTCCATCATGAAGTT CCTGTCCATCATGAAGTT	GCAGTACTCGTCCGCCAT	CGCGTGTCCTGGC CGCGTGTCCTGGC	GCGCCCGAGCTGC	CAGGAGTTCAT(CAGGAGTTCAT(CATCAAGAACCCCGA CATCAAGAACCCCGA
GGGCGCCAACATGC GGCGCCAACATGC	CGAGATCGATGAGCA	CCGCAAGCCTTGGG CCGCAAGCCTTGGG	AGCGCCC	TIGTACGAGCCCAACGG 	;CGGAGCTGCTGCTGGAG CGGAGCTGCTGCTGGAG	;AGAGCCTCAAGGGCA AGAGCCTCAAGGGCA	CGAGGCCACCGGCTA	GAACTACACCGGCG	CATCGGCGTGGGCG CATCGGCGTGGGCG	STCCTTCATGACCG STCCTTCATGACCG	AGGGCGGCTCCGACTTC	CCTTGCCTTTGAGC	CGGCCCCTACAAGGG	TGGACGACGCCGGCAAC	SCTGCCCATCTTCAAGC SCTGCCCATCTTCAAGC	3CAGGCGGTGCGCGAGG 	CGTGCGCCAGCTG GTGCGCCAGCTG
CC 1322 	AC 1262 	AG 1202 	GC 1142 GC 963	GC 1082 	AG 1022 AG 843	AAG 962 AAG 783	AC 902 	TG 842 TG 663	CG 782	AG 722 AG 543	TC 662 	:AG 602 :AG 423	GC 542 	AC 482 	AG 422 AG 243	GTG 362 GTG 183	CTG 302 CTG 123

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This represents the February 3, 2003 version of the continually updated, reviewed, Pseudomonas aeruginosa PAO1 genome annotation, from PseudoCAP (see http://www.pseudomonas.com for latest updates and links to alternate annotations). PseudoCAP is coordinated by
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Pseudomonas aeruginosa PAO1
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
1 (bases 1 to 10.256)
Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P.,
Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J.,
Hickey, M.J., Brinkman, F.S.L., Tolentino, E.,
Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E.,
Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N.,
Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H.,
Wong, G.K.-S., Wu, Z., and Paulsen, I.T.
                                                                                                                              Direct Submission
Submitted (04-FEB-2003) Department of Molecular Biology and
Biochemistry, Simon Fraser University, 8888 University Dr.,
Burnaby, British Columbia V5A 1S6, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete genome sequence of Pseudomonas aeruginosa PA01, opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submission through www.pseudomonas.com of any proposed changes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 t
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2: Function of highly similar gene experimentally demonstrated in another organism (and gene context consistent in terms of pathways its involved in, if known).
3: Function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an experimentally studied gene. Homologs of previously reported genes of unknown function, no similarity to any previously reported sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mkmlkrfivkknergllysbgdflavlepgtyrrfdpydrlsle
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/note="Protein name confidence: Class 4 (homologs of previously reported genes of unknown function, or no
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                                                                                                                                                                                                                                                                                                                   LHTLRQVVCVKG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity to any previously reported sequences)
                                                                                                                                                                                                                                                             locus_tag="PA4584"
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/transI_table=11
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|67. .1312
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'strain="PAO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="GI:9950830"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tocus.
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                                                                                                                                                                                                                            synonym: ycgL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tag="PA4582"
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/Tocus tag="PA4587"
/note="Protein name confidence: Class 1 (function experimentally demonstrated in P. aeruginosa); Subcellular localization
                                                                                                                      /locus_tag="PA4588"
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/note="Protein name confidence: Class 4 (homologs previously reported genes of unknown function, or similarity to any previously reported sequences)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MNREERHPLPAAMRERVLDELERIEREHDVVVLYACESGSRAWGFASPOSDYDVRFVYVHQPEWYQRVEEREDVIERPLSDELDISGWELKKALRLWRKSNPALLEWIGSPLVYREEPLWREELENGSAFHSVPGSRHHYLSMARKNYRGYLKGDSVRLKKKYLYVLKDDSVRLKKYLYVLKDDSVRLKKYLYVLKDDSVRLKKYLYVLKPLFAVRWLDAGLGLPVVAFERLVEATLDDPSLREELDALLSLKRQRDESA
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/note="Protein name confidence: Class
to functionally studied protein)"
                                                                                                                                                                                                                       complement (6156. .7493)
                                                                                                                                                                                                                                                   PASTETTPRPAE"
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                                                                                                                                                                                                                                                                          altapyfhsgqvwelkdavaimgnaqigkqlapddvenivaflhsisgkqprveypli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="ccpR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCCCTCGGTCAACCTCGGGGTGCTGAAGTTCCTCGCCTTCGAGCAGGTCTTCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGCAGATCTTCAAGAAC
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Direct Submission
Submitted (21-OCT-1997)
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/strain="PAO1"
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 GTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATGAGCACGACGCCGAGCTG
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                                                                                        CAGTGGGAATACCTGATGGA---GCTGAAGAACGCTCGCGCCCGGGCATCCGCGAGATGGC
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EMLKUBGRGFDCGRVALSGSGNVAQYAARKVMENGGKVISLSDEGGTLYAEAGLSDEQ
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ANGCVCVAEGANNPSTLEAVDLFLEAGILYAPGKASNAGGVAVSGLENSQNAMRLRENS
EGEVDTKLHGIMQSIHHACLLYGEEQGRVNYVKGANIAGFVKVADAMLAQGVV"
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                                                             /gene="gntK"
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/note="gluconate kina
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/transl_table=11
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Schell, M.A., Karmirantzou, M.,
Pessi, G., Zwahlen, M.-C., Desie
Pridmore, D. and Arigoni, F.
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Schell, M.A., Karmirantzou, M., Snel, B., Vilanova, D., Ber Pessi, G., Zwahlen, M.-C., Desiere, F., Bork, P., Delley, M. Pridmore, D. and Arigoni, F.
The genome sequence of Bifidobacterium longum reflects adaptation to the human gastrointestinal tract
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Bifidobacterium longum NCC2705
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Bifidobacteriaceae; Bifidobacterium.
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complement(160. .525)
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/1.0cu 7903. /gene /1.0cu	gene //gene		ASN			GEEGR 7150.	CKQ MTG KRQ	ADY	/cz /tr	אַל/ מל/ מק/	/tx/	FEA GTA	/1o /no	CDS com	gene com	/tr ASI AVI	ag/ ad/ ad/	/co	CDS com	gene com				/tr SGN Gene Com	dp/ /brc/ /brc/ /brc/	/tr
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Matches

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Query Match
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                                                                    GAACGCCATCAACGTCGAGGTCGTCAAGCAGATCAAGGAAGT
                                                                                                          CAACGGCTTCACGCGCGAGCAGCTGCAGGCGTGCAGGACATGAAGAAGAAGAACAACAG
                                                                                                                                                         TGAGCAGCTGGGCGCCAAGGTCGTCACCGTCTCCGACTCCAACGGCTACATCTACGACCC
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AUTHORS
TITLE
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VERSION
KEYWORDS
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Sequence
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Bifidobacterium longum biovar Longum
Bacteria; Actinobacteria; Actinobacteridae;
Bifidobacteriaceae; Bifidobacterium.
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Location/Qualifiers
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                                                                                                                                            /organism="Bifidobacterium longum biovar Longum"
/mol_type="unassigned DNA"
/db_xref="taxon:1679"
/db_xref="taxon:1679"
/note="1106 seq in place of 1099 because seq 1 (2.256.638
/note="1106 seq in place of 1099 because seq 1001: from
0.000.001 to 0.349.980 length: 349980-seq 1100: from
0.300.001 to 0.649.980 length: 349980-seq 1101: from
0.600.001 to 0.649.980 length: 349980-seq 1102: from
0.900.001 to 0.499.980 length: 349980-seq 1102: from
1.200.001 to 1.249.980 length: 349980-seq 1104: from
1.500.001 to 1.549.980 length: 349980-seq 1105: from
1.500.001 to 1.849.980 length: 349980-seq 1105: from
1.800.001 to 2.149.980 length: 349980-seq 1106: from
1.800.001 to 2.149.980 length: 349980-seq 1106: from
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                                             CATGCCGTCCACCCCGGAGGCCATCGAGGTCTACCAGAAGAACGGCGTGCTGTACGGCCC
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                                                                                                                            TGAGCACGACGCCGAGCTGCTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGCGCCCAA 1315
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                  GGGCGGACTACGCTTCCACCCGACCGTGACCGAGTCCGTCGTCAAGTTCCTTGGCTTCGA
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Bifidobacterium longum biovar Longum
Bacteria, Actinobacteria, Actinobacteridae;
Bifidobacteriaceae; Bifidobacterium.
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Sequence 4 from Patent WO02074798.
AX553950
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The genome of a bifidobacterium
Patent: WO 02074798-A 4 26-SEP-2002;
SOCIETE DES PRODUITS NESTLE S.A. (CH)
                                                                                                                                                                                                                                                                                                                                                                                                               CGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTGGC 364
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                                                                                                            CAACCTGCAGGTCAACCGCGGCTTCCGGCGTGCAGTACTCGGCCATCGGCCCCTACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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/mol_type="unassigned DNA"
/db_xref="taxon:1679"
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Pseudomonas aeruginosa
Bacteria; Proteobacteria;
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CACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGCAGATCTTCAAGAAC
                                                                                                                                                                                                       TTCCTCGAGGCCAACCCGCACTACCTGGAAGCCGGCATCATCGAACGCATCGTCGAACCC
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GTCAAGGTCGCCGATGCGATGCTGGCGCAGGGCGTGGTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGCGCCAACATGCCCTCCACCAACGAG 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGACATCGCCTTCCCCTGCGCCCACCCAGAACGAGATCGAGTGAGCACGACGCCGAGCTG 1274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGCTGCAGGCGGTGCAGGACATGAAGAAGAAGAACAACAGCGCCCGCATCTCCGAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGATCTCGCTGTCCGATTCCGAAGGCACCCTGTATGCCGAGGCGGGGCTCTCCGACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGCTGTCGCTGTCCGACTCCCAGGGCTACGTGTACGAGCCCAACGGCTTCACGCGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACCTTTTCGGCCAGTACAAGCGCATCACCAAGAACTACACGGCGTGCTGACCCCGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCGAGCTGCAGCGCCAC
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                                             ACCAAGGTGGCTGATGCCGTCAAGGCCCCAGGGCGCTGTTTAA 1613
                                                                                               GGGCCGTCCCGCAGATA---CAATGTTGACCTGGCTGCGGGCCCAACATCGCGGGCTTC 1571
                                                                                                                                                                                              CGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTACGACTCCGCCATG
                                                                                                                                                                                                                                                                                             GGCGGGGTGGCGGTGAGCGGTCTGGAGATGTCGCAGAACGCCATGCGCCTGCGCTGGAGC
                                                                                                                                                                                                                                                                                                                                        GGCGGCGTGGCGGTCAGCGGCCTGGAGATGACCCCAGAACCGCATGAGCCTGAACTGGACT 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                     gccarccacaagracaaggccggcarcarcracrgcccggcaaggcggccaacgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCTGGCCAACGGCTGCGTCTGTGTCGCCGAAGGCGCCAACATGCCCTCGACCCTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCGCCCAGGAAATGCTCAAGGATCGTGGCCGCGCTTCGACGGCCAGCGGGTGGCGATC
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RESULT 15 SC0939121

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KEYWORDS
SOURCE
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DEFINITION
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TITLE
JOURNAL
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On or before Oct 30, 2002 this sequence version replaced
gi:3449234, gi:7288050, gi:7320887, gi:7321265, gi:7649562,
gi:8218190, gi:9367445, gi:11544744, gi:20520684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eentley,S.D., Chater,K.F., Cerdeno-Tarraga,A.M., Challis,G.L., Thomson,N.R., James,K.D., Harris,D.E., Quail,M.A., Kieser,H., Harper,D., Bateman,A., Brown,S., Chandra,G., Chen,C.W., Collins,M. Cronin,A., Fraser,A., Goble,A., Hidalgo,J., Hornaby,T., Howarth,S. Huang,C.H., Kieser,T., Larke,L., Murphy,L., Oliver,K., O'Neil,S., Rabbinowitsch,E., Rajandream,M.A., Rutherford,K., Rutter,S., Seeger,K., Saunders,D., Sharp,S., Squares,R., Squares,S., Taylor,K., Warren,T., Wietzorrek,A., Woodward,J., Barrell,B.G., Parkhill,J. and Hopwood,D.A.
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Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 292100)
Bentley, S.D.
Direct Submission
Submitted (09-MAY-2002)
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Streptcomyces coelicolor A3(2) complete genome; segment 18/29.
AL939121 AL031317 AL160431 AL161691 AL161755 AL161803 AL353872
AL356832 AL389898 AL450450 AL451182 AL589164 AL645882
AL939121.1 GI:244429533
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/protein id="CAB77428.1"
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RSSTVPLIKALGWTTEQILERFGEYSSMARTILEKDHTOGUDALLDIYRKLRPGEPFT
REAAQTLLENLYFNPKRYDLAKVGRYKVNKKLGADEPLDAGVLTTDDVIATIKYLVKL
HAGETETVGESGREIVVETDDIDHFGNRRIRNVGELIQNVRTGLARMERVVRERWTT
QDVEAITPQTLINIRPVVASIKEFFGTSQLSOFMDQNNPLSGLTHKRRLNALGPGGIS
RERAGGEVENDHFSHYGRMCPLETFPEGNIGLIGSLASYGRINPFGFIETPYRKVVEG
QVTDDVDYJTADEENRFVIAQANAALGDDMRFAEARRLUTEREGGEVDYVPGDDVJYMD
QVTDDVDYJTADEENRFVIAQANAALGDDMRFAEARRLUTEREGGEVDYVPGDDDVJYMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SCD82.26, rpoB, DNA-directed RNA polymerase beta chain, len: 1161 aa; highly similar to SW:RPOB MYCTU (EMBL:L27989) Mycobacterium tuberculosis DNA-directed RNA polymerase beta chain (EC 2.7.7.6) RpoB, 1178aa; fasta scores: opt: 5849 z-score: 6361.5 E(): 0, 75.7% identity in 1169 aa overlap. Contains Pfam match to entry PP00562 RNA pol_B, RNA polymerase beta subunit and match ot prosite entry PS01166 RNA polymerases beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="synonyms:
111. .3596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Streptomyces coelicolor
/mol_type="genomic DNA"
/strain="A3(2)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ignature"
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// protesin_id="CAD55212.1"
// db_xref="GI:24429534"
// db_xref="GI:200VNFFDELRIGLATADDIRQWSHGEVKKPETINYRTLKPEKD
// tranelation="MLDVNFFDELRIGLATADDIRQWSHGEVKKPETINYRTLKPEKD
// tranelation="MLDVNFFDELRIGLATADDIRQWSHGEVKKPETINYRTLKPEKD
// tranelation="MLDVNFFDELRIGLATADDIRQWSHGEVKPETINYRTLKPEKD
// tranelation="MLDVNFFDELRIGHT"
// tranelation="MLD
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3694. 7593
3694. 7593
/gene="SCO4655"
/note="SCD82.27, rpoC, DNA-directed RNA polymerase beta/
chain (fragment), len: >1058 aa; highly similar to
SW:RPOC_MYCTU (EMBL:L27989) Mycobacterium tuberculosis
DNA-directed RNA polymerase beta/ chain (EC 2.7.7.6) RpoC,
1316aa; fasta scores: opt: 5139 z-score: 5536.5 E(): 0;
72.9% identity in 1067 aa overlap. Contains Pfam match to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCD40A.01, rpoC, DNA-directed RNA polymerase beta' chain (fragment), len: >279 aa; similar to C-terminal region of SW:RPOC BACSU (EMBL:L4359) Bacillus subtilis DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) RpoC, 1199 aa; fasta scores: opt:801 z-score: 911.4 E(): 0; 53.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry PF00623 RNA pol A, RNA polymerase alpha subunit. Contains also possible coiled-coil region aprox. at residues 168. 220
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GQVLESHLIGWLASKGWVSGLAKEEWAQKIQVIGADKVEEGTNVAIPUFDGAREBELAG
LLQHTIPNRDGERMVLPSGKARLFDGRSGEPFPEPISVFMYILKLHHLVDDKLHAKS
TGPYSMITQQPLGGKAQFGGQRRGEMEYWALEAYGAAYALQELLTIKSDDVTGRVKVY
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/gene="SCO4655"
/note="Pfam match to entry PF00623 RNA_pol_A, RNA
polymerase alpha subunit, score 859.20, E-value 1.3e-254"
                                                                                                                                                                                                                                       EVGQKLTVGATNPHDVLRILGQRAVQVHLVGEVQKVYNSQGVSIHDKHIEIIIRQMLR
RVTIIESGDAELLPGELVERTKFETENRRVVQEGGHPASGRPQLMGITKASLATESWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fasta scores: opt:801 z-score: identity in 247 aa overlap"
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/note="PSO1166 RNA polymerases beta chain signature"
3676. .3682
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HEVDARDTKLGPEEITRDIPNVSEEVLADLDERGIIRIGAEVVAGDILVGKVTPKGET
ELTPBERLLAAIFGEKARBVRDTSLKVPHGEIGKVIGVRVFDREEGDELPPGVNQLVR
                                                                                                                                                                                                   SaasfQettrvltdaainaksdsliglkenviigklipagtglsryrnirvepteeak
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                                                                                                                                                           aamysavgyddidyspfgtgsgqavpledydygpynq"
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440 CGTGATCACCTTCCGCGTGTCCTGGCTGGACGACCCGGCAACCTGCAGGTCAACCGCGG
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                                                                                                                                                                                                                                                                               GGCCCAGCCCGAGTTCCACCAGGCGGCCCACGAGGTCCTGGAGACCCTGGCGCCGGTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGAAGCGAGACGCACCCTCGACCACCTCCTCACCGAGATCGAGCTGCGCAACCC
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Streptomyces coelicolor putative integral membrane protein 2SCI34.05, 396 aa; fasta scores: opt: 678 Z-score: 732.5 E(): 3.6e-33; 37.923% identity in 414 aa overlap. Contains possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SCD40A.04, possible glucosyltransferase, len: 345 aa; similar to TR:021943 (EMB:,AF021347) Bacteriophage sfil bactoprenol glucosyl transferase Bgt, 309 a; fasta scores: opt: 728 z-score: 801.5 E(): 0; 39.0% identity in
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9703. .10740
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/transl_table=
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1570 35406	1517 GCCGTCCCGCAGATACAATGTTGACCTGGCTGCGGGCGCCAACATCGCGGGCTT
	457 CGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTACGACTCCGCCATGGG
N UT	397 CGGCGTGGCGGTCAGCGGCCTGGAGATGACCCAGAACCGCATGAGCCTGAACTGGACTCG
υгω	337 CATCCACAAGTACAACCAAGGCCGGCATCATCTACTGCCCCGGCAAGGCGGCCAACGCCGG
1336 35166	277 GATCAAGCACGGCTGCCAGTACGTGGTGGAGGGCGCCAACATGCCCTCCACCAACGAGGC
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1216 35046	157 GAGCGACACCGCCGTGTATGTGGGGGACCGCCGCAAGCCTTGGGAGCTGGACTGCCAGGT
1156 34986	097 GCTGCAGGCGGTGCAGGACATGAAGAAGAAGAACAACAGCGCCCGGATCTCCCGAGTACAA
09 49	037 GCTGTCGCTGTCCGACTCCCAGGGCTACGTGTACGAGCCCAACGGCTTCACGCGCGAGCA
1036 34878	977 TGGCGCGGGCAACGTGGCCCAGTACTGCGGGGGGGCTGCTGCTGGAGGAGGAGGGGCCATCGT
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916 34758	CCAGGAGTATGGCGGCTCCGAGATCCGCCCGAGGCCACCGGCTACGGCGCCGTGCTGTT
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559 34398	00 CTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCTACAAGGGCGGCCTGCGCCTTCCACCC
34338	79 CCAGGTGATGTTCCGGGTGCCGTGGCAGGACGACCAGGGCCGCGTCCGCGTCAACCGGGG

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              Aat64529 NADP-spec
Abk51007 cDNA enco
Aat64542 NADP-spec
Abk51020 NADP-glut
Aat64530 NADP-spec
Abk51020 NADP-spec
Abk51021 NADP-glut
Add36706 NADP-spec
Abk51021 NADP-glut
Add36706 NADP-spec
Aat64531 Glutamate
Abk51009 NADP-glut
Add36708 NADP-glut
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Add36728 NADP-spec
Abk51025 cDNA enco
Aat64548 NADP-spec
Add36728 MATure NA
Aat64548 NADP-spec
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EFFX

DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism plant cells.

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WPI; 19 P-PSDB;	Schmidt	(UYFL	06-OCT-	03-0	10-A	W097	Key CDS transit mat_pep	Ch10	Glut chlo	NADP	17-OCT-	AAT6	RESULT 1 AAT64529 ID AAT6452		4.10						-									
1997-226226/20 DB; AAW15407.	idt RR,	T) UNIV	CT-1995;	03-OCT-1996;	10-APR-1997	WO9712983-A1	nsit_pept	Chlorella so	Glutamate dehydrogenase; chloroplast; transgenic	NADP-specific	OT-2003	4529;	9		435.6	1 4-	447	460.8	467.6	467.6	469.2	472.6	488.6	489.8	499.8	508.2	529.2	590.8 572.4	590.8	1470 =00 0
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end bots out traits a toplated from Chlorella			•	•			lifiers	ď	; NADP-GDH; alga; nitrogen plant; ds.	dehydrogenase alpha-subuni			0 BP.	ALIGNMENTS	AAH68531 AAQ37237	AAF87488	ACA36189	ADS56228	AAF21611	AAA81518	ABZ38921	AAS97271	ACA41075 ABZ38912	AAF87487	ADS58634	ADS45874	ACA27224	ABD05471 ABQ81845	ACA42633	ADQ36730 ARD05527
									n metabolism;	nit precursor cDNA.					Aan68531 C glucami Aaq37237 gdhA gene	Aaf87488 Brevibact	Aca36189 Prokaryot	Ads56228 Bacterial	Aaf21611 Neisseria	Aaa81518 N. mening	Abz38921 N. gonorr	Aas97271 Neisseria	ACA410/5 Prokaryot Abz38912 N. gonorr	Aaf87487 Corynebac	Ads58634 Bacterial Ads61960 Bacterial	Ads45874 Bacterial	Aca27224 Prokaryot	Abd05471 Pseudomon Abq81845 Bifidobac	3	Adg36730 Mature NA

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cDNA clones (AAT64529 and AAT64530) respectively code for the alpha cubunit (AAW15408) precursor proteins of an ammonium-inducible, chloroplast-localised NADP-specific glutamate ammonium-inducible, chloroplast-localised NADP-specific glutamate cammonium-inducible, chloroplast-localised NADP-specific glutamate camponium-inducible, chloroplast-localised NADP-specific glutamate camponium-inducible, chloroplast-localised NADP-specific glutamate camponium-inducible precursor proteins are processed to yield mature alpha and beta subunits (see also AAT64547-48) that comprise the active NADP-GDH capper increasing the assimilation of inorganic N into organic N) by cheef. increasing the assimilation of inorganic N into organic N) by cransforming them with nucleotide sequences encoding the alpha and/or beta subunits. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta cubunits can be expressed that have higher aminating:deaminating activity ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
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The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenae activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield,
                                                                                                            Transforming a plant with a polynucleotide encoding a polypeptide glutamate dehydrogenase activity provides a plant with modulated r metabolism useful to increase yield and ammonium and osmotic stresmetabolism
                                                                        Disclosure; Page 11-13; 35pp; English.
                                                                                                                                                                                                   Schmidt
                                                                                                                                                                                                                                                              01-MAY-1998;
                                                                                                                                                                                                                                                                                      01-MAY-1998;
                                                                                                                                                                                                                                                                                                               23-MAY-2002.
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ammonia toxicity tolerance;
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subunit"
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Best Local Similarity
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DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism

Claim 2; Page 40-41; 61pp; English.

CDNA clones (AAT64542 and AAT64543) respectively code for the alpha subunit (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-inducible, chloroplast-localised NADP-specific glutamate dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They were obtd. by ligation of 3' clone pBGDG53 (AAT64531) and 5' clones pGDG63 (AAT64540) and pGDC64 (AAT64541). The proteins are processed to yield mature alpha and beta subunits (see also AAT64547-48) that comprise the active NADP-GDH hexameric isoenzymes. The nitrogen metabolism of plants can be modulated (pref. by increasing assimilation of inorganic N into organic N) by transforming them with nucleotide sequences encoding the alpha and/or beta subunits. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher capacity for glutamate sinthesis) than homohexamers. (Updated on 17-CCT-2003 to standardise OS eight) synthesis) field)

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                                                                                                                                                                                                                                                Query Match 99.9%;
Best Local Similarity 100.0%;
Matches 2137; Conservative
                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia coxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the coding sequence of Chlorella sorokiniana NADP-glutamate dehydrogenase ligation construct of pBGDC53 plus pGDC63, used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
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DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
                                                                                                                                                                  WPI; 1997-226226/20
                                                                                                                    Claim 2; Page 29-32; 61pp; English.
                                                                                                                                  plant cells.
                                                                                                                                                                               Schmidt RR,
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CC CDNA clones (AAT64529 and AAT64530) respectively code for the alpha CC subunit (AAW15407) and beta subunit (AAW15408) precursor proteins of an CC ammonium-inducible, chloroplast-localised NADD-specific glutamate CC dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They were deposited in CC E. coli DH5alpha as ATCC 69925 and 69926, respectively. The precursor CC proteins are processed to mature alpha and beta subunits (see also CC AAT64547-48) that comprise active NADP-GDH hexameric isoenzymes. The CC nitrogen metabolism of plants can be modulated (pref. increasing the CC assimilation of inorganic nitrogen into organic nitrogen) by transforming CC them with nucleotide sequences encoding the alpha and/or beta subunits. CC Such plants show improved properties, e.g. increased crop yield and CC improved stress tolerance. Heterohexamers having alpha and beta subunits CC can be expressed that have higher aminating deaminating activity ratios CC (i.e. higher capacity for glutamate synthesis) than homohexamers.

Sequence 2099 BP; 416 A; 713 C; 616 G; 354 T; 0 U; 0 Other;

Length 2099;

δ 밁 δ 문 Ś 밁 Ş 밁 Ş Matches Query Match Best Local 241 139 181 121 2098; 79 61 61 _ h 95.6%; Similarity 98.0%; 98; Conservative TCCGCTCCGCCAAGCGCGATGTCCCGCGCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCG 180 CTCCTTTCTGCTCGCCCTCTCCGGTCCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTA 60 CCAAGGCGGGACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGC 300 CGATGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA 240 TCGTGGCC CGATGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA TCCGCTCCGCCAAGCGCGATGTCCGCGCGCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCG 0; Mismatches Score 2046; DB 2; Pred. No. 0; -----TGCGCGTGGG 0 Indels 42; Gaps 198 138 78

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XX Chlc
XX Chlc
XX ET CDS
                                                                                                                     standard;
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cDNA encoding NADP-glutamate dehydrogenase beta subunit.

NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga; nitrogen metabolism; plant; ammonium assimilation; transgenic; ammonia toxicity tolerance; osmotic stress tolerance; gene; ss.

Chlorella sorokiniana

Location/Qualifiers
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/*tag= a
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"NADP-specific glutamate

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Matches 2098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogenabolism useful to increase yield and ammonium and osmotic stress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC cDNA clones (AAT64542 and AAT64543) respectively code for the alpha CC combinit (AAW15407) and beta subunit (AAW15408) precursor proteins of an amnonium-inducible, chloroplast-localised NADD-specific glutamate CC ammonium-inducible, chloroplast-localised NADD-specific glutamate CC dehydrogenase (NADD-GDH) of Chlorella sorokiniana. They were obtd. by CC ligation of 3' clone pBGDc53 (AAT64511) and 5' clones pGDc63 (AAT64540) and pGDc64 (AAT64541). The proteins are processed to yield mature alpha CC and beta subunits (see also AAT64547-48) that comprise the active NADD-CC (CC proteins) by increasing assimilation of inorganic N into organic CC (CC proteins) them with nucleotide sequences encoding the alpha CC and/or beta subunits. Such plants show improved properties, e.g. CC increased crop yield and improved stress tolerance. Heterohexamers having CC alpha and beta subunits can be expressed that have higher capacity for glutamate synthesis) than homohexamers. (Updated on 17-CCT-2003 to standardise OS creatals)
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Best Local Similarity 98.0%;
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P-PSDB; AAW15408.
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GCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGCAGA
                                                                  TGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAAGGGCG
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Pred. No. 0;
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DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism plant cells.

G; 353 T; 0 U; 0 Other; DB 2; 0 Length 2096; Indels 42; Gaps 63

603

498

543 438 423 318 363 303 198

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Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress

Example

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The present invention relates to increasing or decreasing the nitrogen metabolism in plant cells by transforming a plant cell with a polypucleotide encoding a polypeptide having glutamate dehydrogenase (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709), ADQ36731), or their fragments which exhibits GDH activity. The polymucleotide is operably linked to a polymucleotide encoding a chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polynucleotides, and polypeptides are useful in producing plant
                                                                                                                                                                                                                                                                                 Increasing or decreasing nitrogen metabolism in plant cells, for pluvith increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A cDNA clone (AAT64531), designated pBGDC53, was isolated from a Chlorella sorokiniana cDNA library in lambda ZAP by screening with an CADP-specific glutamate dehydrogenase (NADP-GDH) cDNA probe. It comprises the complete 3'-terminal region of the C. sorokiniana NADP-GDH sequence. 5' terminal regions were obtd. by PCR, yielding full-length clones (AAT64542-43) for the alpha and beta subunits of C. sorokiniana NADP-GDH. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glutamate dehydrogenase; NADP-GDH; alga; chloroplast; transgenic plant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 35-36; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sprokiniana algal protoplast(s), useful to modulate nitrogen metabolism
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NADP-glutamate dehydrogenase clone pBGDc53.

RESULT 11
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XX AADPXX NADPXX NADPXX NADPXX OTICIC
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XX PF 01-M3
PR 01-M3 NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga; nitrogen metabolism; plant; ammonium assimilation; transgenic; ammonia toxicity tolerance; osmotic stress tolerance; pBGDc53; gene; ss. Chlorella sorokiniana 01-MAY-1998; 98US-00070844

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Matches 1969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
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The present invention relates to increasing or decreasing the nitrogen metabolism in plant cells by transforming a plant cell with a polypucleotide encoding a polypeptide having glutamate dehydrogenase (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GI (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, ADQ36731), or their fragments, which exhibits GDH activity. The polypucleotide is operably linked to a polypucleotide encoding a chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is usef for increasing or decreasing the nitrogen metabolism in plant cells. The
                                                                                                                                                                                                                                                                 Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
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CGGCTATTTTTTCGCGACGCGCGCCCCCCCGAGAGCCTCTCTCCCCCGAGCCCTAAGC 1860
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RESULT 13
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ID ADQ36723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; NADP-specific GDH; NADP-specific glutamate dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Full-length NADP-GDH cDNA clone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-533134/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SCHM/) SCHMIDT (MILL/) MILLER E
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Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.

Example 2 SEQ ID NO 18; 36pp; English.

The present invention relates to increasing or decreasing the nitrogen cc metabolism in plant cells by transforming a plant cell with a ccomplex polymucleotide encoding a polypeptide having glutamate dehydrogenase cc (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, Cc ADQ36731), or their fragments, which exhibits GDH activity. The cc polymucleotide is operably linked to a polymucleotide encoding a cc chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polymucleotides, and polypeptides are useful in producing plant cc with increased yield, and with improved tolerance to ammonia toxicity, cosmotic stress, and composition of the crop or plant. The present cc sequence is a cDNA clone which was isolated during the isolation of the invention. Sequence analysis revealed cc identified in an example from the invention. Sequence analysis revealed cc all ten clones were identical at their 3' terminian and differed by varying degree of truncation at their 5' terminial clone pBGDc53 (ADQ36712) was the longest clone and was found to have a complete 3' terminus, but was continued to determine the 5' terminal sequence using primers ADQ36713 ADQ36717 and ADQ36718), pRGDc 61 (ADQ36719), pGDc 63 (ADQ36721) and pGDc 64

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904 GCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGACAAGGGCGAGAGGCCTCAAGGGCAAGC 963	28		724 TGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGCCGGCGACATCGGCGTGGGCGGC 783	664 ACCCCAAGGGCAAGAGCGACGCGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCGAGC 723	604 TCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGGCAAGGGCGGCTCCGACTTCG 663	544 GCCTGCGCTTCCACCCCTCGTGAACCTGTCCATGAAGTTCCTTGCCTTTGAGGAG 603	484 TGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAAGGGCG 543	424 TCGTTGAGCCTGAGCGCGTGATCACCTTCCGGGTGTCCTGGCTGG	364 CCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGCAGA 423	304 CCGAGATCTTCATGAAGGACCCGGAGGAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTTGG 363	244 AGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGCTGA 303	184 TGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCACCA 243	124 GCTCCGCCAAGCGCGATGTCCGCGCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCGCGA 183	64 TGGCCGCCCGCTGGCGCACGCCCGCGCTGCCTCGCCCGTGGCCGTGGCCTGGGTCC 123	4.CTTTCTGCTCGCCCTCTCTCCGTCCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTATCG 63	Query Match 79.0%; Score 1691; DB 12; Length 2084; Best Local Similarity 97.5%; Pred. No. 2.8e-270; Matches 2084; Conservative 0; Mismatches 0; Indels 53; Gaps 34;	Sequence 2084 BP; 407 A; 711 C; 614 G; 352 T; 0 U; 0 Other;	7×70003301
Q B Q	Db Qy	B 8	dd VQ	p Q	gg Qg	D QQ	Db Qy	8 8	} B &	B &	}	B 8	₽ \$	2 B 8	B 5	S &	Db	
1984 CGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCAAGTAGCAGTTAGT	1924 CCTGTTGTGAAGCCTACCAGCTCAATTGCCTTTTAGTGTATGTGCGCCCCCCCC	1864 GACGTCCGCCCGACTTTGCCTCGCACATCGCTCGGTTTTGACCCCCTCCAGTCTACCCAC	1804 CTATTITTTCGCGACGCGCGCTCACCCCGACAGCCTCTCCCCCGAGCCCTAAGCGCT 	1744 GCCGTGCCCCTGCAATTCCACCCCAAGAAGAACTAGCGGCACTTGACTGCATCAGGACGG [1642 AAGCGGCCTTTTTCCCAGCCAGGCCCTCACCTGCCCTTCATAACCCTGCTATTGCC	1624 CCCAAGCCACGGCTCACCGGCATCCAACCCAACCAACTCAACGGCCAGGACCTTTTCGG	1564 CGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGGGGGTTTAAGCTGCCCAGG	1504 ACTICGCCATGGGCGTCCGCAGATACATGTTGACCTGGCTGCGGGGGCCAACATG-1468 ACTICGGCCATGGGGGCGTCCGCAGATACAATGTTGACCTGGCTGCGGGGGGCCAACATT	144 TGAACTGGACTCGCAGGAGGTTCGCGACAAGCTGAAGGACATCTACGAGGACATCTACGAGGACATCTACGAGAGAGGACATCATGAAGGACATCTACGAGAGAGGAGGAGAGGAGAGGAGAGAGA	1384 CGGCCAACGCCGGCGGCGGCGGCCAGCAGCGGCCTGGAGATGACCCAGAACGCCATGAG 1352 CGGCCAACGCCGGCGGCGGCGGCGGCCAGCAGCAGACCGCATGAG	1324 CCACCAACGAGCCATCCACAAGTACAACAAGGCCGCATCATCTACTGCCCCGGCAAGTACAACAAGGCCGGCATCATCTACTGCCCCGGCAA 1294 CCACCAACGAGGCCATCCACAAGTACAAGAAGGCCGGCATCATCTACTGCCCCGGCAA 1294 CCACCAACGAGGCCATCGACAAGTACAAGAAGGCCGGCATCATCTACTGCCCCGGCAA	1264 ACGCCGAGCTGATCAAGCACGCTGCCAGTACGTGGTGGTGGAGGGCGCCAACATGCCCT	1204 TGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATGAGCACG	120	062	1024 AGGGGCCATGGTGTCGCTGTCCGACTCCCAGGGCTACGTGTACGAGGCCAACGG 1004 AGGGGGCCATGGTGTCGCTGTCGACTGCCAGGGCTACGTGTACGAGGCCAACGG	946 GCTGCCTGGTGTCTGGCGCGGGCAACGTGGCCCAGTACTGCGCGCGGAGCTGCTGCTGGA	

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RESULT 14
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AD03724
AD03726
CC Polly
CC Chlor
CC Polly
CC Chlor
CC AD0372
CC For
CC Machine
CC AD0372
CC For
CC AD0373
CC Collor
CC Collor
CC AD0373
CC Collor
                                                                                              The present invention relates to increasing or decreasing the nitrogen CC metabolism in plant cells by transforming a plant cell with a CC polynucleotide encoding a polypeptide having glutamate dehydrogenase CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36707), aDQ36729), a beta subunit of NADP-specific GDH (ADQ36709, CC ADQ3671), or their fragments, which exhibits GDH activity. The CC polynucleotide is operably linked to a polynucleotide encoding a CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The cc methods, polynucleotides, and polypeptides are useful in producing plant cc with increased yield, and with improved tolerance to ammonia toxicity, cosmotic stress, and composition of the crop or plant. The present composition of the invention. Ten NADP-GDH clones were identified in an example from the invention. Sequence analysis revealed compositified in an example from the invention. Sequence analysis revealed compositied of an example from the invention. Sequence analysis revealed composition of their 5' termini and differed by varying degree of truncation at their 5' termini and differed by varying degree of truncation at their 5' termini and differed by varying composition of the sound to determine the 5' terminal sequence using primers ADQ36712) was continue, but was not long enough to encode either NADP-GDH subunit and so PCR was carried out to determine the 5' terminal sequence using primers ADQ36713-ADQ36717 and ADQ36721) and the full-length clones ADQ36721) and pgDc 64 (ADQ36722) and the full-length clones ADQ36721 and ADQ36721 and ADQ36722) and the full-length clones ADQ36723 and ADQ36724.
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                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ36724 standard;
                                                                 Sequence 2045 BP;
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GTGCGTGCCTTGCCCTGCCCCGGGATGCGATACTGTGACCTGAGAGTGCTTGTGTA 2103
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                                                                                                                                                                                                                                                                                                                                                                                                                     CTATTTTTTCGCGACGCGCGCTCACCCCGAGAGC--CTCTCCCCCGAGCCCTAAGCGCT
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                                                                                                                                                 CGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGT--CCCCAAGTAGCAGTTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ36712 standard; cDNA; 1922
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Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.

Example 2; SEQ ID NO 7; 36pp; English.

The present invention relates to increasing or decreasing the nitrogen CC metabolism in plant cells by transforming a plant cell with a CC polynucleotide encoding a polypeptide having glutamate dehydrogenase CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, CC ADQ36701, or their fragments, which exhibits GDH activity. The CC polynucleotide is operably linked to a polynucleotide encoding a CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their CC fragments that exhibit chloroplast transit activity. The method is useful CC for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polynucleotides, and polypeptides are useful in producing plant CC sequence is a cDNA clone which was isolated during the isolation of the sequence is a cDNA clone which was isolated during the isolation of the ADDP-specific GDH cDNAs of the invention. Ten NADP-GDH clones were conducted and their 3' termini and differed by varying CC all ten clones were identical at their 3' termini and differed by varying CC degree of truncation at their 5' termini. Clone pBGDc53 (ADQ36712) was cont long enough to encode either NADP-GDH subunit and so PCR was carried out to determine the 5' terminal sequence using primers ADQ36713-ADQ36717 cand ADQ36719, pRGDc 61 (ADQ36719), pGDc 63 (ADQ36721) and pGDc 64 (ADQ36722) and the full-length clones ADQ36721 and ADQ36723 and ADQ36723 and ADQ36723 and ADQ36724.

Sequence 1922 BP; 393 A; 638 C; 567 G; 324 T; 0 U; 0 Other;

δ Query Match
Best Local Similarity
Matches 1922; Conserv CAGATCTCCGCGATGGACGCCACCACCGCGACTTCACGGCGCTGCAGAAGGCGGTGAAG Conservative 73.1%; 0, Pred. No. 1.800; Mismatches Score 1565; DB 12; Pred. No. 1.8e-249; Indels 47; Gaps 230

CAGATICTCCGCGATGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAG

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1310 1119	1 ATCGATGAGCACGACGCCGAGCTGCTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGC	
1250 1061	0	
1190 1003	131 AACAGCGCCCGCATCTCCGAGTACAAGAGCGACACCGCCGTGTATGTGGGCGACCGCCGC	
1130 945	1071 GAGCCCAACGGCTTCACGCGCGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAAC	
1070 886	1011 CTGCTGCTGGAGAAGGGCGCCATCGTGCTGTCGCTGTCCGACTCCCAGGGCTACGTGTAC	
1010 827	51 CTCAAGGGCAAGCGCTGCCTGGTGTCTTGGCGCGGGCAACGTGGCCCAGTACTGCGCGGAG	
950 768	AGA 	
890 709	1 TACACCGGCGTGCTGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAG	
830 650	71 GGCGTGGGCGCGCGCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAAC	
770 591	711 TTCATGACCGAGCTGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGCCGGCGGCACATC	
710 532	1 GGCTCCGACTTCGACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCC	
650 473	591 GCCTTTGAGCAGATCTTCAAGAACAGCCTGACCATCCCTGCCCATGGGCGGCGAGGGCAAGGGC	
590 414	531 CCCTACAAGGGCGGCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTT	
530 355	71 GACGCCGGCAACCTGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCCGTCCG	
47 0 296	411 ATCTTCAAGCAGATCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGCTGG	
410 237	351 GTGCGCGAGGTGGCCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCC	
350 178	91 CGCCAGCTGCTGACCGAGATCTTCATGAAGGACCCGGI 	
290 119	231 CAGATGGCCACCAAGGCGGGCACTGACGGCCTGGTGCACGGCATCAAGAACCCCGACGTG	

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	1201, Ap		479, App	_	1438, Ap	2485, Ap	21, Appl	16, Appl	16, Appl	13, Appl	13, Appl	4059, Ap	1828, Ap	1, Appli	1, Appli	e 137, App	2, Appli	1 1 1 1

ALIGNMENTS

RESULT 1 US-08-541-033A-1

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US-08-541-033A-1
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 2140; Conservative 0
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
                                                                                                                                                                                                                                                                                               TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYP
TITLE OF INVENTION: RELATING TO
TITLE OF INVENTION: DEHYDROGENA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                        MOLECULE TYPE: CDNA
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LENGTH: 2140 base pairs
                                                                                                                                                  FEATURE:
                                                                                                        NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                           STRANDEDNESS:
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33..1610
                                                                                                                                                                                         linear
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RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
                                            Score 2140;
                                            DВ
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                                       Length 2140;
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Mismatches 0

Indels

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Gaps

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Pred. No.

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1081 GCTTCACGCGCGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAAGAACAACAGCGCCC 1140

RESULT 2

301 TGACCGAGATCTTCATGAAGGACCCGGAGCAGGAGTTCATGCAGGCGGTGCGCGAGG		QY 181 CGATGGACGCCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA 240	Qy 121 TCCGCTCCGCCAAGCGCGAATGTCCGCGCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCG 180	Qy 61 TCGTGGCCCCCCGCTGGCGGCACGCCCCGCGCTCGCGCCGTGGCCCGTGGCGCGTGGG 120	CCTTTCTGCTCGCCCTCTCTCCGTCCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTA 60	Query Match 100.0%; Score 2140; DB 2; Length 2140; Best Local Similarity 100.0%; Pred. No. 0; Matches 2140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Y: CDS	nucleic acid DNESS: doub Y: linear TYPE: cDNA	; TELEFAX: (904) 372-5800 ; INFORMATION FOR SEQ ID NO: 1: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 2140 base pairs	REGISTRATION NUMBER: 36,965 REFERENCE/DOCKET NUMBER: UF155 TELECOMMUNICATION INFORMATION: TELECHONE: (904) 375-8100	APPLICATION NUMBER: US/08/541,033 FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Whitlock. Ted W.	APPLICATION NUMBER: US/08/828,451 ; FILING DATE; ; CLASSIFICATION: ; PRIOR APPLICATION DATA;		., _ ພ ≺	ADDRESSEE: Saliwanchik & Saliwanchik ; STREET: 2421 N.W. 41st Street, Suite A-1 ; CITY: Gainesville ; STATE: Florida	RELATING TO THE - AND -SUBUNITS OF G DEHYDROGENASES AND METHODS OF USE : 26 ESS:	GENERAL INFORMATION: APPLICANT: Schmidt, Robert R. APPLICANT: Miller, Philip TITLE OF INVENTION: NOVEL POLYPEPTIDE	US-08-828-451-1 ; Sequence 1, Application US/08828451 ; Patent No. 5985634
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1381 AGGCGGCCAACGCCGGCGGCGGCGGTCAGCGGCCTGGAGATGACCCAGAACCGCATGA 1440	1321 CCTCCACCAACGAGGCCATCCACAAGTACAACAAGGCCGGCATCATCTACTGCCCCGGGA 1380	1261 ACGACGCCGAGCTGCTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGCGCCAACATGC 1320 1261 ACGACGCCGAGCTGCTGATCAAGCACGGCTGCCAGTACGTGGAGGGCGCCAACATGC 1320	OI AGCINGACIONACIONACIAN ACCINICACIONE CONTROLLA CONTROL	41 GCATCTCCGAGTACAAGAGCGACACCGCCGTCTTATGTGGGCGACCGCCGCAGCCTTGGG	1081 GCTTCACGCGCGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAAGAACAACAGCGCCC 1140	1021 AGAAGGGCCCATCGTGCTGTCCGTGTCCGACTCCCAGGCTACGTGTACGAGCCCAACG 1080	961 AGCGCTGCTGGTGTCTGGCGCGGGCAACGTGGCCCAGTACTGCGGGGAGCTGCTGG 1020	901 ACGGCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGACAAGGGCGAGAGCCTCAAGGGCA 960 	841 TGCTGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGCT 900	781 CGCGCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAACTACACCGGCG 840	721 AGCTGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGGCGGACATCGGCGTGGGCG 780	661 TCGACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCG 720	601 AGATETTEAAGAACAGEETGACEACCTGCECATGGGCGGCGAAGGGCGGCTCCGAET 660	541 GCGGCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCAAGTTCCTTGCCTTTGAGC 600	481 ACCTGCAGGTCAACCGCGGCTTCCGGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAAGG 540	421 AGATCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGCTGG	361 TGGCCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCCATCTTCAAGC 420	301 TGACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGG 360

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GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

APPLICANT: Schmidt, Philip

ITILE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE

TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: Florida
COUNTRY: USA

ZIP: 32606
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US-08-541-033A-18
; Sequence 18, Application
; Patent No. 5879941
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Whitlock, Ted W.
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 065
REFERENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 2137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2137 base pairs
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TOPOLOGY: lir
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STRANDEDNESS: double
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	1803	1744 GCCGTGCCCCTGCAATTCCACCCCAAGAAGAACTAGCGGCACTTGACTGCATCAGGACGG	
	1743 1740	684 AAGCGGCGCCTTTTTCCCAGCC	
	1683 1680	24 CCCAAGCCACGGCTCACCGGCAATCCAAC 	
	1623 1620	564 CGGGCTTCACCAAGGTGGCTGATGG	
	1563 1560	504 ACTCCGCCATGGGGCCGTCCCCGCAGATACAATGTTGACCTGGCTGCGGGCCCC 	
	1503 1500	1444 TGAACTGGACTCGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTACG	<u>.</u> .
•	1443 1440	384 CGGCCAACG 381 CGGCCAACG	
	1383 1380	324 CCACCAACGAG	
	1323 1320	264 ACGCCGAGCTGCTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGCGCCAACAT	
	1263 1260	1204 TGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATGAGCACG	
	1203 1200	1144 TCTCCGAGTACAAGAGCGACACCGCCGTGTATGTGGGGCGACCGCCGCAAGCCTTGGGAGC	
	1143 1140	1084 TCACGCGCGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAAGAACAACAGCGCCCGCA	
	1083 1080	1024 AGGGCGCATCGTGCTGTCGCTGTCCGACTCCCAGGGCTACGTGTACGAGCCCAACGGCT	
	1023 1020	964 GCTGCCTGGTGTCTGGCGCGGGCAACGTGGCCCAGTACTGCGCGGAACCTGCTGCTGGAGA	
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	903	44 TGACCCCGAAGGGCCAGGAGT	
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STREET: 4241 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION NUMBER: US/08/828,451
FILING DATE:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
APPLICATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELEOMOUNICATION INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: UF155
TELEOMOUNICATION INFORMATION:
TELEPAN: (904) 375-8000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARROTERISTICS:
LENGTH: 2137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPPOLOGY: linear
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US-08-828-451-18
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                                                                            ; MOLECULE TYPE: US-08-828-451-18
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Patent No. 5985634
GENERAL INFORMATION:
Query Match 99.9%; Score 2137; 1
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2137; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schmidt, Robert R. APPLICANT: Miller, Philip TITLE OF INVENTION: NOVEL POLITICE OF INVENTION: RELATING TITLE OF INVENTION: DEHYDROGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
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                                      DB 2;
                                      Length 2137;
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPAX: (904) 375-8100
TELEPAX: (904) 375-8100
TELEPAX: (904) 375-8100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2099 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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US-08-541-033A-3
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Best Local Similarity
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APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GI
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE 26
CORRESPONDENCE AND METHODS OF USE
CORRESPONDENCE 36

CORRESPONDENC
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                          ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite CITY: Gainesville STATE: Florida COUNTRY: USA ZIP: 32606
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REFERENCE/DOCKET NUMBER: UF15:
TELECOMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPACNE: (904) 372-8800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2099 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity 98.0%;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Query Match Best Local Similarity

95.5%;

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No. 0;

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Length 2096;

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US-08-41-033A-19

US-08-41-033A-19

; Sequence 19, Application US/08541033A

; Patent No. 5879941
STRANDEDNESS: don
TOPOLOGY: linear
MOLECULE TYPE: CDN
US-08-541-033A-19
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MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
FILING
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APPLICANT: Schmidt, Robert R.

APPLICANT: Miller, Philip

AND POLYNUCLEOTIDES

TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GI

TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26
                                                                                                                                                                                          TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 2421 N.W. OF CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 32606
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CGAATTTTCCTGCCATGAGACGTGCGGGTTCCTAGCCTGGTGACCCAAGTAGCAGTTAGT	CTATTTTTTTCCCGACCGCGCTCACCCCGAGACCCTCTCTCCCCCGAGCCCTAAGCCCT GACGTCCGCCCGACTTTGCCTCGCACATCGCTCGGTTTTGACCCCCTCCAGTCTACCCAC	AAGCGGCGCCTTTTTCCCAGCCAGGGCCCTCACCTGCCCTTTCATAACCCTGCCTG	CGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAAGGGGGCTGTTTAAGCTGCCCAGGCCCAAGGAGCACTGATGAAGCTGCCCAGGCCAAGGAAGG	TGAACTGGACTCGCGAGGAGGTTCGCGACAAGCTGGAGGAGCGCATCATGAAGGACATCTACG ACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTTGCGGGGCGCACAATCTACG ACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTTGCGGGCGCCAACATCG ACTCCGCCATGGGCCGTCCCGCAGATACAATGTTGACCTGGCTTCGGGGCGCCAACATCG CGGGCTTCACCAAGGTGGCCGCAGATACAATGTTGACCTAGGGCGCTTTTAAGCTGCCCAGG	CCACCAACGAGGCATCCACAAGTACAACAAGGCCGGCATCACTCTACTGCCCCGGCAAGGCCACCAACGACGAGGCCATCAAGGCCCGCATGAGGCCGGCC	TGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCAGAACGAGATCGATGAGCACG ACGCCGAGCTGGATCAACAAGCACGGCTGCCAGTACGTGGGGGGGG	TCACGCGCGAGCAGCTGCAGGGGGTGCAGGACATGAAGAAGAAGAACAACAGCGCCCGCA
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELEFAX: (904) 372-8800
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2096 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                        Matches 2095;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Patent No. 5985634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2421 N.W. CITY: Gainesville
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STREET: 2421 N.W. 41st Street, Suite A-1
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RESULT 9
US-08-541-033A-7
                                                                                                                                                                                                                                                               Sequence 7, Application US/08541033A Patent No. 5879941 GENERAL INFORMATION:
                                                                                                                                                       APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GI
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                      STATE: F
                                                                                                  ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
CITY: Gainesville
STATE: Florida
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 372-8000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
Matches 1969; Conserv
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APPLICATION NUMBER: US.
FILING DATE:
CLASSIFICATION: 435
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Patent No. 5985634
GENERAL INFORMATION:
                                                                                                                                                                                                     Matches 1969;
                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 2421 N.W. 41st Street: CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Whitlock, Ted W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLI
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/828,451 FILING DATE:
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                   ilarity 100.0%;
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100.0%; Pred. No. 0;
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US-08-541-033A-23 (US-08-541-033A-23) (Patent No. 5879941 (Patent No.	Db 1261 AACCCCTAAGCCTGAACTGGACTCCCCAAGAAGAACTAAGCCTCTCCCCCG 1850 OY 1491 AAGCACATCAAGACTCGACCTCGCCATGGGGCCCTCCGGAAACAATCCATATGCCTTCGCCAACAACCCGCATCAATG 1320 1491 AAGCACATCTACGACTCCGCCATGGGGCCGTCCCGGAAATCCAATGTTGACCTTGGCTGGC

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Query Match
Best Local Similarity
Matches 1502; Conserv
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 1506 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1506 base pair
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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LOCATION:
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Pred. No. 1.8e-295;
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| Sequence 23, Application US/08828451 |
| Patent No. 5985634 |
| GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Schmidt, Robert R. APPLICANT: Schmidt, Philip |
| ITILE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES |
| TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAM |
| TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE |
| NUMBER OF SEQUENCES: 26 |
| CORRESPONDENCE ADDRESS: ADDRESSEE: Saliwanchik & Saliwanchik |
| STREET: 2421 N.W. 41st Street, Suite A-1 |
| CITY: Gainesville |
| STATE: Florida
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US-08-828-451-23
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CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: US/08/541,
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WHITION UNMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.9%;
Matches 1502; Conservative
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/828,451
FILING DATE:
FILING DATE:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                        CTGTCCATCATGAAGTTCCTTGCCTTTGAGCAGATCTTCAAGAACAGCCTGACCATGAACATCATGAACATCCTTGAGCATGATCATGAAGTAGTTCCTTGCCTTTGAGCAGATCTTCAAGAACAGCCTGACCATGAACAGTCCTTGAGCAGATCTTCAAGAACAGCCTGACCACTG
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                                CCCATGGGCGGCAAGGGCGGCTCCGACTTCGACCCCAAGGGCCAAGAGCGCGACGCGAG
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Pred. No. 1.8e-295;
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RESULT 13
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; Sequence 25, Application US/08541033A
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603 809 663 869 723 723 929 929 989

Qy 423 ATCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGCTGG	Qy 303 ACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTG 362	Oy 183 ATGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCCC 242	S-08 Que Bes	; TYPE; nucleic acid ; STRANDEDNESS: double ; TOPOLOGY: linear ; MOLECULE TYPE: CDNA	TELECOMMUNICATION INFORMATION: TELEPHONE: (904) 375-8100 TELEPAX: (904) 375-8000 INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:	; AFFLICATION NUMBER: US/08/541,U33A ; FILING DATE: CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION: ; NAME: Whitlock, Ted W. ; REFERENCE/DOCKET NUMBER: UF155 ; REFERENCE/DOCKET NUMBER: UF155	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DO SOFTWARE: PatentIn Release #1. CURRENT APPLICATION DATA:		GENERAL INFORMATION: APPLICANT: Schmidt, Robes APPLICANT: Miller, Philit TITLE OF INVENTION: NOVEL TITLE OF INVENTION: RELATI TITLE OF INVENTION: DEHYI NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
B & B & B &	}	S B S B S	? B Q B 4	\$ B Q	Q Db	Q Db Q	P	S B S	Q D Q Db
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RESULT 14
US-08-828-451-25
; Sequence 25, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
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APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLECTIDES
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF GLUTAM
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
COURRENT APPLICATION DATA:
APPLICATION 
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Best Local Similarity
Matches 1470; Conserva
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                    GCCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGCAG
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GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: AUGUEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUGUEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: AUGUEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: AUGUEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: AUGUEIC STORE DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 1099-02-18
PRIOR APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION SEQ ID NOS: 33142
SEQ ID NO 4131
LENGTH: 1497
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4131
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GGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGCTACGGCGCCCGTGCTG 914
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Search completed: July Job time: 388 secs 9, 2005, 23:47:31

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11159.130 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/2/pubpna/US07
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'Cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:
'Cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
'Cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
'Cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
'Cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
'Cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
'Cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
'Cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
'Cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
'Cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
'Cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:
'Cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:
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'Cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
'Cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
'Cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
'Cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
'Cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US06
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!_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

Score	Query Match	Length	BB	ID	Description
2140	100.0		9	US-09-070-844-1	Sequence 1, Ap
2140	100.0		19	US-10-627-886-1	Sequence 1, A
2137	99.9		9	US-09-070-844-18	Sequence 18, A
2137	99.9		19	US-10-627-886-18	Sequence 18,
2046	95.6		φ	US-09-070-844-3	Sequence 3, Ap
2046	95.6		19	US-10-627-886-3	Sequence 3, A
2043	95.5		9	US-09-070-844-19	Sequence 19, Appl
	Score 2140 2140 2137 2137 2046 2046 2043		Query Match Length 100.0 2140 100.0 2137 99.9 2137 99.9 2137 95.6 2099 95.6 2099 95.5 2096	Match Length D 100.0 2140 100.0 2140 99.9 2137 99.9 2137 95.6 2099 95.6 2099 95.6 2099	Query Match Length I 100.0 2140 100.0 2140 99.9 2137 99.9 2137 99.6 2099 95.6 2099 95.5 2096

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US-10-282-122A-42104	US-10-369-493-44956	US-10-472-928-4979	US-10-158-844-137	US-08-961-527-137	US-10-282-122A-37840	US-10-282-122A-12258	US-10-282-122A-17814	US-10-282-122A-7100		US-10-369-493-33526	10-28	US-09-980-217-1	US-10-282-122A-39409	US-10-369-493-32481	US-10-282-122A-19460	US-09-738-626-3482	09-738-	2-122	10-42	US-10-369-493-31902			-10-28	•	US-10-369-493-34308	-SD	US-10-282-122A-3135	us-	US-10-470-565-1		-886-	US-09-070-844-25	US-10-627-886-23	US-09-070-844-23	US-10-627-886-7	09-070-844-7	US-10-627-886-19
Sequence 42104, A	14956,	e 49	Sequence 137, App	137,	equence		Sequence 17814, A	e 7100,	æ		369	Sequence 1, Appli	39		e 1946(3482, A	1, Ap	24059,		31902		151,	28945,	37634,		24304,	31354,	150	e	3050	e 25,	25,	e 23,	23,	e 7,	7, 7	Sequence 19, Appl

ALIGNMENTS

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US-09-070-844-1

(Sequence 1, Application US/09070844

(Patent No. US2002062495A1

(PAPLICANT: MILLER, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: Florida

COUNTRY: USA
ZIP: 33606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER DEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER PAPLICATION DATA:
APPLICATION NUMBER: US/09/070,844

FILING DATE:
CLASSIFICATION NUMBER: 08/725,596

FILING DATE:
FILING DATE:
FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic scid
STRANDEDNESS: double
TOPOLOGY: linear
NOISELLE TYPE: CENT
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LOCATION:
JS-09-070-844-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2140; Conservative 0; Mismatches
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RESULT 2
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                                                                                                                                                TELEPHONE: (352) 37
TELEFAX: (352) 372-
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                               APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: L10yd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 32606-6669
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PAtentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MILLE, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES
RELATING TO THE .-
                                                 TOPOLOGY: line, MOLECULE TYPE: cDNA
                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
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LOCATION:
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                                                                                  TYPE: nucleic acid STRANDEDNESS: double
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ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELEPAX: (904) 375-8100
TELEFAX: (904) 375-8100
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-070-844-18
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US-09-070-844-18
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Patent No. US20020062495A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOT
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 2137; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VCURRENT APPLICATION DATA:
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ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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STATE: Florida
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NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-CITY: Gainesville STATE: Florida COUNTRY: USA ZIP: 32606-6669
                                                                                                 APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBUNITS OF G:
DEHYDROGENASES AND METHODS OF USE
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INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 2137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO
US-10-627-886-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.9%; Score 2137; [Best Local Similarity 100.0%; Pred. No. 0; Matches 2137; Conservative 0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: CUnknown>
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APPLICATION UNMBER: 09/070,844

FILING DATE: 01-MAY-98

APPLICATION NUMBER: 08/725,596

FILING DATE: 03-OCT-96

APPLICATION NUMBER: 08/541,033

FILING DATE: 06-OCT-95

APPLICATION NUMBER: 08/541,033

FILING DATE: 06-OCT-95

APPLICATION NUMBER: 05/541,033

FILING DATE: 06-OCT-95

ATTORNEY/ACENT INFORMATION:

NAME: L10yd, Jeff
REGISTRATION NUMBER: 35,599

REFERENCE/DOCKET NUMBER: UF-155CD3

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TELEPAX: (352) 372-5800
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                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

APPLICANT: Miller, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GI

TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEB: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
TELECOMMUNICATION INFORMATION: TELEPHONE: (904) 375-8100 TELEFAX: (904) 372-5800
                                              ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                        CITY:
STATE:
                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
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Best Local Similarity
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                                                                                                  GCTGACGTCCGCCGACTTTGCCTCGCACATCGCTCGGTTTTGACCCCCTCCAGTCTACC
                                                                                                                                                                                                                                         GCCGCCGTGCCCCTGCAATTCCACCCCAAGAAGAACTAGCGGCACTTGACTGCATCAGGA 1800
                                                                                                                                                                                                                                                                                                                    CGGAAGCGGCGCCTTTTTTCCCAGCCAGGCCCTCACCTGCCCTTTCATAACCCTGCTATT
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                                                            GCTGACGTCCGCCCGACTTTGCCTCGCACATCGCTCGGTTTTGACCCCCCTCCAGTCTACC
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Query Match
Best Local Similarity
Matches 2098; Conserv
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                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARES: PatentIn Release #1.0, Vers
SOFTWARES: PatentIn Release #1.0, Vers
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
APPLICATION NUMBER: 05/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (352) 375-800
TELEPHONE: (352) 375-800
                                                                         NAME/KEY: CDS
LOCATION: 33..1568
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
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MEDIUM TYPE: Floppy disk
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                                                                                                                         FEATURE:
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STATE: Florida
COUNTRY: USA
ZIP: 32606-6669
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TYPE: nucleic acid
STRANDEDNESS: double
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   Conservative
              95.6%;
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Pred. No. 0;
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7	RESULT	1081 GCTTCACGCGCGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAAGAACAACAGCGCCC 1140
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AGTGT	}	961 AGCGCTGCTGGTGTCTGGCGCGGGCAACGTGGCCCAGTACTGCGCGGAGCTGCTGGTGCTGG 1020
CCCCGAATTTTCCTGCCATGAGACGIGCGGTTCCTAGCCTGGTGACCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTTGGTGACCCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTTGGTGACCCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTTGGTGACCCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACCTGGAGACCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCATGAGACCTGAGACCTCAAGTAGCAGTT CCCCGAATTTTTCCTGCCATGAGACCTGGAGACCTCAAGTAGCAGTT CCCCCGAATTTTCCTGCCATGAGACCTGAGACAGTAGAACCCCCAAGTAGCAGTT CCCCGAATTTTCCTGCCAAGTAGAACACAAGTAGAACAAGTAGAACAAGTAGAAAAAAAA	?	901 ACGGCGCCGTGCTGTTTGTGGAGAAACGTGCTGAAGGACAAGGGCGAGAGCCTCAAGGGCA 960
CACCCTGTTGTGAAGCCTACCAGCTCAATTGCCTTTTAGTGTATGTGCGCCCCCTCCTGCTGCTGCTGCTGTTGAAGCCTACCAGCTCAATTGCCTTTTAGTGTATGTGCGCCCCCTCCTGC	. B. &	841 TGCTGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGCT 900
GCTGACGTCCGCCCGACTTTGCCTCGCACATCGCTCGGTTTTGACCCCCCTCCAGTCTACC	. dd .	781 CGCGCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAACTACACCGGCG 840
GGCTATTTTTTTGCGGACGCGCTCACCCCGAGAGCCTCTCCCCCGAGCCCTAAGC	° ₽. \$	721 AGCTGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGCCGGCGACATCGGCGTGGGGG 780
GCGCCGTGCCCCTGCAATTCCACCCCAAGAAGAACTAGCGGCACTTGACTGCATCAGGA	B &	661 TCGACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTTGCCAGTCCTTCATGACCG 720
GGAAAGCGGCGCTTTTTCCCAGCCAGGGCCTCACCTGCCCTTTCATAACCCTGCTATT	. B &	601 AGATCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGGCAAGGGCGGCTCCGACT 660
AGGCCCAAGCCACGGCTCACCGGAATCCAACCCAACCAAC) B 8	541 GCGGCCTGCGCTTCCACCCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGC 600
St. TOGOGGOTTCACCAAGGIGGCTGATGCCGTCAAGGCCCTAGGGGCCTGTTTAAGCTGCCC	?	481 ACCTGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAAGG 540
SUI ACGACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGCGGGCGCCAACA	}	421 AGATCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGACGACGACGCCGGCA 480
9CC16) B &	361 TGGCCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGC 420
AGGCGGCCAACGCCGGCGGCGTGAGCGGTCAGCGGGCCTGGAGATGACCCAGAACCGCATGA	, p 64	301 TGACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGG 360
00100	, B &	241 CCAAGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGC 300
	}	181 CGATGGACGCCACCGCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA 240
AGCTGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATC) B &	121 TCCGCTCCGCCAAGCGCGATGTCCGCCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match '
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 2095; Conservative
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELECHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite CITY: Gainesville
STATE: Florida
COUNTRY: USA
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APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GITTLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
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                                                 CCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTGG
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0; Mismatches
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RESULT 8
US-10-627-886-19
US-10-627-886-19
; Sequence 19, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
 MILIER, Philip
; APPLICANT: Schmidt, Robert R.
 Miller, Philip
; TITLE OF INVENTION: ROVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE - AND -SUBUNITS OF GI
NEHYDROGENASES AND METHODS OF USE
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COUNTRY: USA

COUNTRY: USA

ZIP: 32606-6669

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAtentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/10/627,886
                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSES: Saliwanchik
STREET: 2421 N.W. 41st
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 26
CORRESPONDENCE APPROVE
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Best Local Similarity
Matches 2095; Conserv
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APPLICATION UNMBER: 09/070,844

FILING DATE: 01-MAY-98

APPLICATION NUMBER: 08/725,596

APPLICATION NUMBER: 08/541,033

FILING DATE: 06-OCT-96

APPLICATION NUMBER: 08/541,033

FILING DATE: 06-OCT-95

ATTORNEY/AGENT INFORMATION:

NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589

REFERENCE/DOCKET NUMBER: UF-155CD3

TELEPHONE: (352) 375-8100

TELEPHONE: (352) 372-5800
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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID
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CLASSIFICATION: <Unknown>
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	1564 CGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGGGGCTGTTTAAGCTGCCCAGG 1623	
	1504 ACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGCGGGCGCCAACATCG 1563	
	1444 TGAACTGGACTCGCGAGGAGGTTCGCGACAAGCTGGAGGCGCATCATGAAGGACATCTACG 1503 	
	1384 CGGCCAACGCCGGCGGCGGGGGTCAGCGGCCTGGAGATGACCCAGAACCGCATGAGCC 1443	
	1324 CCACCAACGAGGCCATCCACAAGTACAAGAGGCCGGCATCATCTACTGCCCCGGGCAAGG 1383	
	1264 ACGCCGAGCTGCTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGGGCCAACATGCCCT 1323	
	1204 TGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCAGAACGAGATCGATGAGCACG 1263	
	1144 TCTCCGAGTACAAGAGCGACACCGCCGTGTATGTGGGGCGACCGCCGCAAGCCTTGGGAGC 1203 	
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ט ג	1024 AGGGCGCCATCGTGCTGTCCGACTCCCACGGCTACGTGTACGAGCCCAACGGCT 1083	
S B 8	964 GCTGCCTGGTGTCTGGCGCGGGCAACGTGGCCCAGTACTGCGCGGAGCTGCTGCTGCAGAA 1023 	
5 B &	904 GCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGACAAGGGCGAGAGCCTCAAGGGCAAGC 963 	
S B &	844 TGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGCTACG 903	
S B 8	784 GCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAACTACACCGGCGTGC 843 	
S & &	724 TGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGCCGGCGACATCGGCGTGGGCGCGC 783	
S B 8	664 ACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCGAGC 723	

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CLASSIFICATION:
PRIOR APPLICATION UMBER: 08/725,59
APPLICATION NUMBER: 08/725,59
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEG ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 base pairs quence 7, Application US/09070844

tent No. US20020062495A1

ENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHTDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26 COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CONTROLLED STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: cDNA CORRESPONDENCE ADDRESS: STATE: Flor COUNTRY: US ZIP: 32606 CITY: Gainesville STATE: Florida TYPE: nucleic acid STREET: ADDRESSEE: 2421 N.W. USA Saliwanchik & Saliwanchik 21 N.W. 41st Street, Suite 08/725,596 UF155 A-1 #1.25

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 AACAGCGCCCGCATCTCCGAGTACAAGAGCGACACCGCCGTGTATGTGGGCGACACCGCCGC
                        GGCTCCGACTTCGACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCC
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RESULT 10
US-10-627-886-7
; Sequence 7, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; Miller, Philip
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CCCTACAAGGGCGGCCTGCGCTTCCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTT	471 GACGCCGGCAACCTGCAGGTCAACCGGCGCTTCCGCGTGCAGTACTCGTCCGCCATCGGC	QY 411 ATCTTCAAGCAGATCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGGTCGAGC 470	Qy 351 GTGCGCGAGGTGGCCGTCTCCCTGCAGCCCGTGTTCGAGAAAGCGCCCCGAGCTGCTGCCC 410	Oy 291 CGCCAGCTGCTGACCGAGATCTTCATGAAGGACCCGGAGCAGGAGTTCATGCAGGCG 350	QY 231 CAGATGGCCACCAAGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTG 290	CCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGG	Query Match 92.0%; Score 1969; DB 19; Length 1969; Best Local Similarity 100.0%; Pred. No. 0; Matches 1969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-10-627-886-7	; SEQUENCE CHARACTERISTICS: ; LENGTH: 1969 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: double	; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (352) 375-8100 ; TELEPAX: (352) 372-5800 ; INFORMATION FOR SEO ID NO: 7:	ATTORNEY/AGENT INFORMATION: ; NAME: Lloyd, Jeff ; REGISTRATION NUMBER: 35,589 ; REFERENCE/DOCKET NUMBER: UF-155CD3	APPLICATION NUMBER: 08/725,596 ; FILING DATE: 03-OCT-96 ; APPLICATION NUMBER: 08/541,033 ; FILING DATE: 06-OCT-95	CLASSIFICATION: <unknown> PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/070,844 FILING DATE: 01-MAY-98</unknown>	SOFTWARE: PatentIn Release #1.0, Version #1.25; CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/627,886 FILING DATE: 24-Tul-2003	COMPUTER READABLE FORM: COMPUTER: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC DOS/MS-DOS		; NUMBER OF SEQUENCES: 26 ; CORRESPONDENCE ADDRESS: ; ADDRESSE: Saliwanchik & Saliwanchik ; STREET: 2421 N.W. 41st Street, Suite A-1	TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES RELATING TO THE AND -SUBUNITS OF GLUTAMATE DEHYDROGENASES AND METHODS OF USE
9	QQ da	9d 4	S B 7	5 8 7		Qy dd	Db Oy	Qy	Db	D Qy	Qy	Db Qy	Qy dd	D Qy	Db Qy	Qγ	Db	סס
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Sequence 23, Application US/09070844

Patent No. US2002062495A1

GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
ITILE OF INVENTION: RELATING TO THE '- ANI
ITILE OF INVENTION: DEHYDROGENASES AND ME:
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-:
COUNTRY: USA
COUNTRY: USA
ZIP: 32606
COMPUTERE DEADABLE FORM.
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US-09-070-844-23
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
APPLICATION NUMBER: 08/725,596
FILING DATE:
APPLICATION NUMBER: 36,965
REGISTRATION NUMBER: 36,965
REGISTRATION NUMBER: 36,965
REGISTRATION NUMBER: UF155
TELECOMMUNICATION:
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-8800
INFORMATION FOR SEQ ID NO: 23:
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Best Local Similarity
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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LOCATION:
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          GTGGCCCAGTACTGCGCGGAGCTGCTGCTGGAGAAGGGCGCCATCGTGCTGTCGCTGTCC
                                                       CTGAAGGACAAGGGCGAAGCCTCAAGGGCAAGCGCTGCCTGGTGTCTGGCGCGGGCAAC
                                                                                                                                  GGCTCCGAGATCCGCCCCGAGGCCACCGGCTACGGCGCCGTGCTGTTTGTGGAGAACGTG
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                                                                                                                                                                                         TACAAGCGCATCACCAAGAACTACACCGGCGTGCTGACCCCGAAGGGCCAGGAGTATGGC
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Pred. No. 0;
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RESULT 12
US-10-627-886-23
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23, Application US/10627886 Publication No. US20040128710A1 GENERAL INFORMATION:
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 33606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Ver
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES RELATING TO THE .- AND -SUBUNITS OF GLEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schmidt, Robert R.
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Best Local Similarity 99.:
Matches 1502; Conservative
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1506 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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APPLICATION NUMBER: 09/070,844

FILING DATE: 01-MAY-98

APPLICATION NUMBER: 08/725,596

FILING DATE: 03-0CT-96

APPLICATION NUMBER: 08/541,033

FILING DATE: 06-0CT-95

ATTORNEY,AGENT INFORMATION:
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LOCATION: 4..1464
SEQUENCE DESCRIPTION: SI
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REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
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Pred. No. 0;
0; Mismatches
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RESULT 13
US-09-070-844-25
; Sequence 25, Application US/09070844
; Patent No. US20020062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND TITLE OF INVENTION: RELATING TO THE '- AND
                                                                                                                                                                                                                                                                                                               GTCAAGGCCCAGGGCGCTGTTTAAGCTGCCCAGGCCCAAGCCACGGCTCACCGGCAATCC 1649
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Best Local Similarity
Matches 1470; Conserv
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1473 base pair
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REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
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STRANDEDNESS: double
TOOLCGY: linear
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  ATCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGGCAAGGGCGGCTCCGACTTC
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                                                                                                                    GCGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGCGCTGTTTAAGCCTGCCCAG 1622
                                                                                                                                                                                                           GACTCCGCCATGGGGCCGTCCCCGCAGATACAATGTTGACCTGGCTGCGGGGCGCCAACATC
                                                                                                                                                                                                                                                                                               CTGAACTGGACTCGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTAC
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           GCCCAAGCCACGGCTCACCGGCAATCCAAC 1473
                                                                                                                                                                                  GACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGCGGGCGCCCAACATC
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, NAME/KEY: CDS
; LOCATION: 4..1431
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-627-886-25
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                                                                                                                                                                                                                                                                                                                         Query Match 68.7%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                        Matches 1470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (352) 372-5800 INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-0CT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-0CT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTERATION NUMBER: 35,589
REGISTERATION NUMBER: UF-155CD3
TELEPERNUMICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-UL1-2003
CLASSIFFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                      363
                                                                             124
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     184
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                                                                                                                                                                                                                                                                      183 ATGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCACC
                                                                                                                                                       64
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STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Gainesville
STATE: Florida
COUNTRY: USA
                             GCCGTCTCCCTGCAGCCCCGTGTTCGAGAAAGCGCCCCGAGCTGCTGCCCATCTTCAAGCAG
                                                                           ACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTG
                                                                                                       ACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTG
                                                                                                                                                      AAGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGCTG
                                                                                                                                                                                                                                ATGGACGCCACCACCAGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCACC
       GCCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCCATCTTCAAGCAG
                                                                                                                                                                                           AAGGCGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1473 base pairs
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                           Score 1470;
; Pred. No. 0;
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GACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGCGGGCGCCAACATC
                                                                                               GCGCCAACGCCGGCGGCGTGGCGGTCAGCGGCCTGGAGATGACCCAGAACCGCATGAGC
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APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Garn
APPLICANT: Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
APPLICANT: NUMBER: 00/10/282,122A
CURRENT APPLICATION NUMBER: 60/20,200
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2000-10-2-2
PRIOR APPLICATION NUMBER: 60/269,308
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US-10-282-122A-30503
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3503
LENGTH: 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30503, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Pseudomonas
                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1384
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                                                381
                                                                                                                                        321 GACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGGAGGTGGCCGTCTCCCTGCAGCCC
                                                                                                                                                                                                                     887;
TTCCTCGAGGCCAACCCACACTACCTGGAAGCCGGCATCATCGAACGCATCGTCGAACCC
                                             GTGTTCGAGAAGCGCCCCGAGCTGCTG-----CCCATCTTCAAGCAGATCGTTGAGCCT
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                                                                                                      GATCCCGATCAGCCCGAATTCCACCAGGCGGTGGAAGAGGTGCTGCGTTCCCCTCTGGCCG
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                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                   27.6%;
                                                                                                                                                                                                                                                                                                                                                    aeruginosa
                                                                                                                                                                                                            Score 590.8; DB 17;
Pred. No. 1.5e-132;
0; Mismatches 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See File Wrapper or PALM
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                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                               Length 1338;
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5 CGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTACGACTCCGCCATG 1514	59 €
5 GGCGGCGTGGCGGTCAGCGGCCTGGAGATGACCCAGAACCGCATGAGCCTGAACTGGACT 1454	ര ഒ
5 GCCATCCACAAGTACAAGAAGACGGCGATCATCTACTGCCCCGGCAAGGCGGCCAACGCC 1394 	$\alpha - \alpha$
5 CTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGGCCCAACATGCCCTCCACCAACCA	1275 CT 997 CT
5 GTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATGAGACGACGACGCCGAGCTG 1274	1215 GT 940
5 AAGAGCGACACCGCCGTGTATGTGGGCGACCGCCGCAAGCCTTGGGAGCTGGACTGCCAG 1214	1155 AA 883 GC
5 CAGCTGCAGGCGGTGCAGGACATGAAGAAGAAGAACAACAGCGCCCGCATCTCCGAGTAC 1154	1095 CA 826 CA
5 GTGCTGTCGCTGTCCGACTCCCAGGGCTACGTACGAGCCCAACGGCTTCACGCGCGAG 1094	1035 GT 766 GT
TCTGGCGCGGCAACGTGGCCCAGTACTGCGCGGAGCTGC	QQ
5 TTTGTGGAGAACGTGCTGAAGGACAAGGGCGAGAGCCTCAAGGGCAAGCGCTGCCTGGTG 974	15 TT 46 TT
5 GGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGCTACGGCGCCGTGCTG 914	გ—გ
5 TACCTTTTCGGCCAGTACAAGGCCATCACCAAGAACTACACCGGCGTGCTGACCCCGAAG 854	D D
5 ATCAGCTACGTGCAGGACGTGCCCGCCGGCGGCGACATCGGCGTGGGCGCGCGAGGATTGGC 794	735 AT 466 GT
5 AAGAGCGACGCGAAGGTGATGCGCTTCTGCCAGTCCTTCATGACCGAGCTGCAGCGCCAC 734	675 AA 406 AA
5 AGCCTGACCACCCTGCCCATGGGGGGGGGGCAAGGGGGGGTTCCGACTTCGACCCCAAGGGC 674	615 AG 346 TC
5 CACCCCTCCGTGAACCTGTCCATGAAGTTCCTTGCCTTTGAGGAGATCTTCAAGAAC 614	$\Delta - \Delta$
5 CGCGGCTTCCGCGTGCAGTACTCCGTCCGCCATCCGGCCCTACAAGGGCGGCCTGCGCTTC 554	495 CG 226 CG
GAGCGCGTGATCACC	435 GA 166 GA

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Search completed: July 10, 2005, 00:07:50 Job time: 1216 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                             source
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510 CAGTACTCGTCCGCCATCGGCCCCTACAAGGGCGGCCTGCGCTTCCACCCCTCCGTGAAC 569
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                                                                                                                                                                                                                                                                                                                                                             Email: craymond@u.washington.edu
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                               University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 206216954
Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1245)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sime,E.E., Hastings,M.,
Spencer,D.H., Kaul,R. and Olsen,M.V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                        TTCCGCGTGTCCTGGCTGGACGACGCCGGCAACCTGCAGGTCAACCGCGGCTTCCCGCGTG
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                                                                                                     Conservative
                                                                                                                                                                                        library."
                                                                                                                                                                                                      /clone="pacs2-164 965"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                                                                                                                                          db_xref="taxon:287"
                                                                                                                                                                                                                                                                                          organism="Pseudomonas"
mol_type="genomic DNA"
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pacs2-164_965.s2 pacs2-164 Pseudomonas aeruginosa genomic clone
pacs2-164_965, genomic survey sequence.
BZ569676
BZ569676.1 GI:27204626
                                                                                University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 206216954
Fax: 2066857244
                                                                                                                                                 Contact: Chris K. Raymond Genome Center
                                                                                                                                                                             Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Burns,J.L., Kaul,R. and Olsen,M.V. Whole-Genome-Sequence variation among multiple isol Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                          (bases 1 to 1123)
                                                                 craymond@u.washington.edu
                                                   shotgun
                                    Location/Qualifiers
/organism="Pseudomonas aeruginosa"
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/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
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/strain="2-164"
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Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M., Burns,J.L., Kaul,R. and Olsen,M.V.
Whole-Cenome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
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Similarity 72.2%;
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GCTGCTGCTGGAGAAGGGCGCCATCGTGCTGTCGCTGTCCGACTCCCAGGGCTACGTGTA 1069
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/clone="msh2_5687"
/clone_lib="msh"
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/strain="MSH"
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Pred. No. 4.1e-61;
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Best Local Similarity
Matches 520; Conserv
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EST879285 non-normalized T1 cDNA library Trichomonas vaginalis cDNA
clone TVTCY21 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: carlton@tigr.org
Seq primer: lambda TriplEx2.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Jane Carlton
Parasite Genomics Group
Parasitute for Genomic Research
The Institute for Genomic Rockville,
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other_ESTs: EST879284
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carlton,J.M., Dyall,S., Johnson,P.J. and Fraser,C.M.
The complete genome sequence of the sexually transmitted parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trichomonas vaginalis
Eukaryota; Parabasalidea; Trichomonada; Trichomonadida;
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CV219575.1
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Fax: 301-838-0208
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                                                                                                                                                                      GTGATCACCTTCCGCGTGTCCTGGCTGGACGACGCCGGCAACCTGCAGGTCAACCGCGGC
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                     TCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGCAGATCTTCAAGAACAGCCTG
                                                                                                TTCCGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAAGGGCGGCCTGCGCTTCCACCCC
                                                                                                                                                                                                                      ATCCTTGAGAAGGAACCAAAGTATCAGAAGCTCCTCCCAGCCCTCGTTGAACCAGAACGT 177
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AACGTTAACCTTTCCATCCTCAAGTTCCTTGGCTTCGAGCAAGTTTTCAAGAACTCACTT
                                                                                                                                                 GTTATCATGTTCCGTGTCCCATGGGTTAACGACAAGGGTGAGATGATGGTCAACCGTGGC
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                                                                       TTCCGTGTCCAATTCAACTCCGCAATTGGCCCATACAAGGGTGGTTGCCGTTTCCGTGGC
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                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: Lambda TriplEx2; Site_1: SfiA; Site_2: SfiB; T. vaginalis strain T1 library constructed from SfiB; T. vaginalis strain T2 library constructed from CDNA, made in lambda TriplEx2. Inserts cloned unidirectionally in the SfiA and SfiB sites. Mass excision of library produced inserts in pTriplEx2 plasmid. Inserts sequenced from both 5' and 3' ends using TriplEx2 sequencing primer and polydT 24 bp primer respectively."
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/clone_lib="non-normalized T1 cDNA library"
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Pred. No. 1.6e-59;
0; Mismatches 283;
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                                                                                                                                                                                          Carlton, J.M., Dyall, S., Johnson, P.J. and Fraser, C.M. The complete genome sequence of the sexually transmitted Trichomonas vaginalis Unpublished (2004) Other ESTS: EST870778 Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                     Trichomonas vaginalis
Trichomonas vaginalis
                                                                                                                                                                                                                                                                                                                                                    CV211069
EST870779 non-normalized clone TVTBE13 5' end, mRN CV211069
                                                                                                                                                        Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                          CV211069.1
                                                                                                                                                                                                                                                                             Eukaryota; Parābasalidea; Trichomonada; Tricho
Trichomonadidae; Trichomonadinae; Trichomonas
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                                                                                                                                                                                                                                                                    (bases
                                                                                              il: carlton@tigr.org
primer: lambda TriplEx2.
    Location/Qualifiers
                                                                                                                                   301-530-9319
/db xref="taxon:5722"
/clone="TVTBE13"
/clone_lib="non-normalized T1 cDNA library"
/clone_TVector: Lambda TriplEx2; Site_1: SfiA;
                                                 /mol_type="mRNA"
/strain="T1"
                                                                         organism="Trichomonas"
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                                              T3 end of clone AWOAA009C04 of library AWOAA
Yarrowia lipolytica, genomic survey sequence.
AL411141
AL411141.1 GI:12180271
GSS.
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           Yarrowia lipolytica
Yarrowia lipolytica
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
   Saccharomycetales; Dipodascaceae; Yarrowia.
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Query Match
Best Local Similarity
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exignus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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                                           CTGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAAGGGC 542
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/strain="CLIB 89"
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                                                                                                                                                                                   Sakyo-ku, Kyoto, Ky
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BW480553 Nori Satoh unpublished cDNA library, mature animal Ciona intestinalis cDNA clone cima038a08 5', r
                                                                                                                                                                                                                                                               Unpublished (2004)
Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 854)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                Ciona intestinalis
Ciona intestinalis
                                                                                                                                            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                              Kyoto University
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Urochordata; Phlebobranchia; Cionidae; Ciona.
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                                                                /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/tissue_type="whole animal"
/dev_stage="mature adult"
                                              clone="cima038a08"
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CV211068 943 bp mRNA linear EST 16-SEP-
EST870778 non-normalized T1 cDNA library Trichomonas vaginalis
clone TVTBE13 3' end, mRNA sequence.
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CV211068.1 GI:52158048
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Unpublished (2004)
Other ESTs: EST870779
Contact: Jane Carlton
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Carlton, J.M., Dyall, S., Johnson, P.J. and Fraser, C.
The complete genome sequence of the sexually trans
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301-530-9319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: carlton@tigr.org
Seq primer: polydT 24 base.
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ACCGCCGTGTATGTGGGCGACCGCCGCAAGCC---TTGGGAGCTGGACTGCCAGGTGGAC
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                                                                                                                                                                                                                                                                                                                                                      GGCTCCGAGATCCGCCCGAGGCCACCGGCTACGGCGCCGTGCTGTTTGTGGAGAACGTG
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                                                   ATGCACATCAAGAACGTTGCTCGTACAGAACTCAAGAAGATTTCAGAACTCTTCCCAGAC
                                                                                     CAGGACATGAAGAAGAAGAACAACAGCGCCCGC----ATCTCCGAGTACAAGAGCGAC
                                                                                                                      GACTCACACGGCGCTCTCATCTTCAAGGATGGTATGACAAAGGAGCATCTTGATGCTGTC
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/clone lib="non-normalized T1 cDNA library"
/clone lib="non-normalized T1 cDNA library"
/clone lib-"non-normalized T1 library Site_1: SfiA; Site_2:
/note="Vector: Lambda TriplEx2; Site_1: SfiA; Site_2:
SfiB; T. vaginalis strain T1 library constructed from
cDNA, made in lambda TriplEx2. Inserts cloned
unidirectionally in the SfiA and SfiB sites. Mass excision
of library produced inserts in pTriplEx2 plasmid. Inserts
sequenced from both 5' and 3' ends using TriplEx2
sequencing primer and polydT 24 bp primer respectively."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="T1"
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The First Laboratory for Plant Gene
Kazusa DNA Research Institute
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Porphyra yezoensis
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                                 GACGACGCCGGCAACCTGCAGGTCAACCGCGCGTTCCGCGTGCAGTACTCGTCCGCCATC 527
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GATGACGCGGGGGAGCTGCAAGTCAACCGCGGCTTCCGCGTGCAGATGAACTCTGCGCATT
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                                                                                                                                                                                                                                                                                                      1532-3, Kisarazu, Chiba 292-0812, Japan
l: asamizu@kazusa.or.jp, URL:http://www.l
Location/Qualifiers
                                                                       Conservative
                                                                                                                                                          /clone="PF005c01_r"
/dev_stage="sporophytes"
/clone_lib="Porphyra yezoensis TU-1 sporophytes"
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/mol_type="mRNA"
/strain="TU-1"
                                                                                                                                                                                                                   db_xref="taxon:2788"
                                                                                      13.2%;
                                                                     Score 282.8; DB 1
Pred. No. 4.6e-46;
0; Mismatches 157
                                                                                                                                                                                                                                                                                                                           URL: http://www.kazusa.or.jp/en/plant/.
                                                                                                     DB 1;
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Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 820)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R. J. AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
                                                                                                                                                                               Seq primer: T7
Class: fosmid
                                                                                                                                                                                                               Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  survey sequence.
CL693787
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Spemannstr. 37-39, Tuebingen
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                                                                                                                                                                                                                                                                        Fax: 00497071601498
                                                                                                                                                                                                                                                                                         Tel: 00497071601371
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                                                                                                                                                                             fosmid ends
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var. California"
                                                                                                     /organism="Pristionchus
/mol_type="genomic DNA"
                /note="Vector: pEpifos-5
                                                                                                                                                            Location/Qualifiers
                                                                                        strain="California"
                                                                                                                                             . 820
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JOURNAL COMMENT
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Tyler,B. Not Published
Unpublished (2003)
Contact: Tyler B
Tyler lab
                                                                                                                                                                                                                      CF839891 638 bp mRNA linear EST 30-OCT-200 psHB004xF07f USDA-IFAFS:Expression of Phytophthora sojae genes during infection and propagation_sHB Phytophthora sojae cDNA clone
                                                                                                                                                                           sHB004F07 5, mRNA sequence.
CF839891
CF839891.1 GI:38055545
                                                                Tyler,B.
                                                                                               Phytophthora.
                                                                                                              Eukaryota; stramenopiles;
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                                                                                                              Oomycetes; Pythiales; Pythiaceae;
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Plate: 004 row: F column: 07
Seq primer: BK reverse primer
High quality sequence stop: 638
Location/Qualifiers
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Tel: 540-231-7318
Email: bmtyler@vt.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR PRimers
FORWARD: BK reverse primer
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                   CAGTGGCACCGTGGCGCTCAACGTGGCCCCAGAAGCTGCT
                                               CGCGGGCAACGTGCCCAGTACTGCGGGAGCTGCTGCT 1018
                                                                               CAACCGCATCCTGGAGACGCGGAGAGACGCTCAAGGGCAAGCGCTGCCTGATCTCGGG
                                                                                                       GGAGAACGTGCTGAAGGACAAGGGCGAGAGGCCTCAAGGGGCAAGCGCTGCCTGGTGTCTGG
                                                                                                                                               GGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGCTACGGCGCCGTGCTGTTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="mycelium"
/cell_line="p6497"
/dev_stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone lib="USDA-IFAFS.Expression of Phytophthora sojae
genes during infection and propagation_sHB"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xho1"
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/mol_type="mRNA"
/db_xref="taxon:67593"
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Pred. No. 2e-44;
0; Mismatches 204;
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365 739 305 679 248 619 188 559 128 499 89 439 N

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Department of Zoology
Kyoto University
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1 (bases 1 to 727)
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                                                                                                                                                                                            TIGCCTTIGAGCAGATCTTCAAGAACAGCCTGACCACCCTGCCCAIGGGCGGCGGCAAGG
                                                                                                                                                                                                                                                                     eccccracaaeeecceccrececrrccacccrccereaaccrercarcareaaerrcc
                                                                                                                                                                                                                                                                                                                                                                       CAGTTTTGCCAGCAGTGTGCGAGCCAGAAAGGGTGGTACAATTCCGAGTACCATGGCAGG
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TCGGCGTGGGCGCGCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGA
                               GCTTCATGACGGAGTTGTTCAAACACATTGGCCCGGATACCGACGTCCCCGCTGGAGATA 491
                                                           CCTTCATGACCGAGCTGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGCCGGCGACA
                                                                                                 GTGGGTGCGATTTTGATCCAAAGGGAAAAACTGACAGCGAAGTTCTCAGGTTTTGCCAGA
                                                                                                                               GCGGCTCCGACTTCGACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGT 708
                                                                                                                                                                   TGGGCTTCGAGCAAATATTTAAGAACGCACTCACGACACTTCCAATGGGAGGCGGCAAAG
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81-75-705-1113
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"

/db_xref="taxon:7719"
/clone="cijv033107"
/tissue_type="whole animal"
/dev_stage="juvenile"
/clone_lib="Nori Satoh unpublished cDNA library,
whole animal"
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/mol_type="mRNA"
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61.2%;
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Pred. No. 8.1e-44;
0; Mismatches 277;
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                                                                                                                                                                                                                                                                                                                    423;
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Department of Zoology
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Expressed genes in Ciona
Unpublished (2004)
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Ciona intestinalis
Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 81-75-753-4081 Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502,
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CCCTCCGTGAACCTGTCCATGAAGTTCCTTGCCTTTGAGCAGATCTTCAAGAACAGC
                                                                     GGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAAGGGCGGCCTGCGCCTTCCAC
                                                                                                                                                                                   CCGTTATTCGATCGCTACCCCAAGTACTTGTCAGTTTTTGCCAGCAGTGTGCGAGCCAGAA 131
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                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cijv403b07"
/tissue_type="whole animal"
/dev_stage="juvenile"
/clone_lib="blori Satoh unpublished cfwhole animal"
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Pred. No. 1.7e-43;
0; Mismatches 259;
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Best Local Similarity
Matches 434; Conserv
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 22
                                                                                                                                                                                                                                                                                                                                 Sakyo-ku, Kyoto, Kyoto 606-8502,
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 730)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2004)
Unpublished (2004)
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Department of Zoology
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                              TGCGCCAGCTGCTGACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGG
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   TGGACGAAGTGCAAGCTAAAGTACGAAGCAGGGATCCAAACCAAACTGAGTTTTTGCAGG
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                                                               Conservative
                                                                                                                                                                                                                                                                                                               satoh@ascidian.zool.kyoto-u.ac.jp
                                                                                                                                                /dev_stage="mature adult"
/clone_lib="Nori Satoh unpublished
adult whole animal"
                                                                                                                                                                                                                               /organism="Ciona intestinalis"
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/db_xref="taxon:7719"
                                                                                                                                                                                                /clone="cima014f19"
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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Pred. No. 2.7e-43;
0; Mismatches 275;
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Asamizu,E., Nakajima,M., Kitade,Y., Saga,N., Nakamura,Y. and Tabata,S.
COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS
                                                                                                             OF PORPHYRA YEZOENSIS (RHODOPHYTA FREQUENCY ANALYSIS
J. Phycol. 39 (5), 923-930 (2003)
Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                               AU196696
AU196696 Porphyra yezoensis TU-1 sporophytes Porphyra yezoensis CDNA Clone PFL093d06_r 5', mRNA sequence.
                           The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL:http://www.l
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/organism="Porphyra yezoensis"
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Search completed: July 9, 2005, 23:40:56 Job time : 6266 secs
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/db_xref="ttaxon:2788"
/clone="PFL093d06_r"
/dev_stage="sporophytes"
/clone_lib="Porphyra yezoensis TU-1 sporophytes"
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Adq36709 NADP-spec
Aau98954 Mature NA
Adq36729 Mature NA
Aaw15411 NADP-spec
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Aaw15413 Mature NA
Adq36731 Mature NA
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Adq36731 Mature NA
           Ads24914
Adn27186
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Aau98950 NADP-spec
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26
1201	1201	1204	1205.5	1205.5	1207.5	1210.5	1211.5	1212	1214	1221	1230	1230.5	1234.5	1236.5	1238	1238	1239	1239.5	1239.5
44.2	44.2	44.3	44.3	44.3	44.4	44.5	44.5	44.6	44.6	44.9	45.2	45.2	45.4	45.5	45.5		45.6	45.6	456
447	447	447	444	424	464	458	448	448	448	448	449	449	448	449	449	449	449	448	448
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ABU15360	AAW60830	AAW08092	ABU20518	ADN17964	ABU23354	ADS28251	ADH97149	ABU01740	ABU46100	ADK47974	ABU38946	ABU44405	ADH85999	ABP28423	ABU30172	AAB88536	AAU91467	ADH97147	ABU29386
Abu15360	Aaw60830	Aaw08092	Abu20518		Abu23354	Ads28251	Adh97149	Abu01740	Abu46100		Abu38946	Abu44405	_	-	Abu30172	Aab88536	Aau91467	Adh97147	Abu29386
Protein e	E. coli g	Glutamina	Protein e	Bacterial	Protein e	Bacterial	E. faecal	S. pneumo	Protein e	Streptoco	Protein e	Protein e	Enterococ	Streptoco	Protein e	Haemophil	Haemophil	B. faecal	Protein e

ALIGNMENTS

RESULT 1 AAW15407 ID AAW1 Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism; chloroplast; transgenic plant. WO9712983-A1. NADP-specific glutamate dehydrogenase alpha-subunit precursor AAW15407 standard; protein; 526 06-OCT-1995; 03-OCT-1996; Chlorella sorokiniana; strain UTEX 1230. 17-OCT-2003 10-JUL-1997 AAW15407; 10-APR-1997. (revised) (first entry) 95US-00541033. 96WO-US015921. ₿

Schmidt RR, N-PSDB; AAT64529, AAT64542. WPI; 1997-226226/20. (UYFL) UNIV FLORIDA. Miller P;

DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism plant cells.

Claim 1; Page 25-27; 61pp; English.

2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-inducible, chloroplast-localised NADP-specific glutamate dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha and beta subunits (see also AAW15401-12) that comprise the active NADP-GDH hexameric isoenzymes. The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAW16429-30, AAW16417-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta

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RESULT 2
AAU9899
XX AAU9899
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  (SCHM/)
                                                                                                                                                                                                                                                                                                                 NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; nitrogen metabolism; plant; ammonium assimilation; transgenic; ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
                                                                         01-MAY-1998;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
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                                                         VAXO
                                                                        QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page
                                                                                                                                                                       XDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ
                                                                                                                                                                                      KDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ
                                                                                                                                                                                                                              VPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVL
                                                                                                                                                                                                                                                                                        SIMKFLAFEQIFKNSLTTLEMGGGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQD
                                                                                                                                                                                                                                                                                                                                               RPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNL
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                                                                                                               DMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGC
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; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to increasing or decreasing the nitrogen CC metabolism in plant cells by transforming a plant cell with a CC polynucleotide encoding a polypeptide having glutamate dehydrogenase CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, CC ADQ36731), or their fragments, which exhibits GDH activity. The CC (ADQ36731), or their fragments, which exhibits GDH activity. The CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their CC fragments that exhibit chloroplast transit activity. The method is useful CC for increasing or decreasing the nitrogen metabolism in plant cells. The CC methods, polynucleotides, and polypeptides are useful in producing plant CC sequence.is the precursor protein of the crop or plant. The present CC sequence is the precursor protein of the alpha subunit of the NADP-specific GDH, which is then processed to produce the mature alpha subunit of the NADP-specific GDH, used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; SEQ ID NO 2; 36pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schmidt RR, Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1998;
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                                                                                                                                                           RPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNL 180
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VPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVL
                                                                                                                                                                                                                                                                  MQTALVAKPIVAAPLAARPRCLAPWPCAWVRSAKRDVRAKAVSLEEQISAMDATTGDFTA
                                                      SIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQD
                                                                                       SIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQD 240
                                                                                                                       RPELLPIPKQIVEPERVITERVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNL
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tive 0;
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Pred. No. 1.3e-250;
Mismatches 0;
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                                                         2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-inducible, chloroplast-localised NADP-specific glutamate dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha and beta subunits (see also AAW15411-12) that comprise the active NADP-GDH hexameric isoenzymes. The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAT64529-30, AAT64547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher aminating deaminating activity ratios (i.e. higher capacity for glutamate synthesis) than homohexamers. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
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Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrometabolism useful to increase yield and ammonium and osmotic stress
                                                                                                                                            tolerance.
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Claim 6; Page 17-18; 35pp; English.

The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana NADP-glutamate dehydrogenase beta subunit, used in the method invention

Sequence 512 AA;

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NADP-specific GDH beta subunit precursor protein, SEQ ij

Nitrogen metabolism; plant; beta subunit; NADP-specific

glutamate dehydrogenase; GDH; GDH; NADP-specific glutamate

dehydrogenase enzyme;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                Score 2621; DB.8;
Pred. No. 3.6e-241;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   512;
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Matches

41 Ŋ

AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ 100

AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ

61

Query Match Best Local Similarity

92.2%;

0

Score 2508; DB 5; Pred. No. 2.1e-230; 0; Mismatches 0;

Length Indels

0;

Gaps

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                                           The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynuclectide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana mature NADP-glutamate dehydrogenase alpha subunit, used in
 Sequence 487 AA;
                                                                                                                                                                                                                                               Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
                                                                                                                                                                                                                                                                                                                WPI; 2002-499691/53.
N-PSDB; ABK51025.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlorella sorokiniana
                                                                                                                                                                                                     Claim 7; Page 27-28; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002062495-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nitrogen metabolism; plant; ammonium assimilation; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mature NADP-glutamate dehydrogenase alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU98954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU98954 standard;
                                                                                                                                                                                                                                                                                                                                                                                              (SCHM/) SCHMIDT R R. (MILL/) MILLER P.
                                method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tolerance; osmotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stress tolerance; enzyme
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RESULT 8
ADQ36729
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AC ADQ3
AC ADQ3
AC ADQ3
AC ADQ3
AC ADQ3
AC Matu
XX Matu
XX Mitr
XX Mitr
XX Chlo
PN US20
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                                                           Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
                                                                                                                                                                                                                                                                                                                                                           Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme; alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
                                                                                                                              WPI; 2004-533134/51.
N-PSDB; ADQ36728.
                                                                                                                                                                                                                                                                                                                                                                                                  Mature NADP-specific GDH alpha subunit, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ36729 standard; protein; 487
                                      Claim 7; SEQ
                                                                                                                                                                   Schmidt
                                                                                                                                                                                           (SCHM/)
                                                                                                                                                                                                                                01-MAY-1998;
                                                                                                                                                                                                                                                         24-JUL-2003; 2003US-00627886
                                                                                                                                                                                                                                                                                   01-JUL-2004.
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                                                                                                                                                                                                                                                                                                                                   Chlorella sorokiniana.
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MILLER P.
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                                   ID NO 24; 36pp; English.
                                                                                                                                                                  Miller
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The present invention relates to increasing or decreasing the metabolism in plant cells by transforming a plant cell with a

RESULT 9
AAW15411
ID AAW15411
AC AAW1
XX AW1
AC AAW1
XY 17-C
DT 10-J
XX W 10-J
XX W Glut
XW Glut
XW Glut
XX Chlc
XX Chlc

Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;

dehydrogenase alpha subunit

plant

Chlorella sorokiniana; strain UTEX 1230

chloroplast; transgenic

17-OCT-2003 10-JUL-1997

(revised)
(first entry) glutamate

AAW15411;

AAW15411 standard; protein; 487

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide encoding a polypeptide having glutamate dehydrogenase (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, ADQ36731), or thair fragments, which exhibits GDH activity. The polynucleotide is operably linked to a polynucleotide encoding a chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polynucleotides, and polypeptides are useful in producing plant with increased yield, and with improved tolerance to ammonia toxicity, osmotic stress, and composition of the crop or plant. The present sequence is the mature alpha subunit of the NADP-specific GDH used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 487 AA;
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                                                                          GLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV
                                                                                                                                       CATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
                                                                                                                                                                                                     SQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKFWELDCQVDIAFF
                                                                                                                                                                                                                                                                                                                              MRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
                                                                                                                                                                                                                                                                                                                                                                                                                             QEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQ
KAQGAV
                            KAQGAV
                                                          GLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV
                                                                                                                       CATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
                                                                                                                                                                                   SOGYVYEPNGFTREQLOAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP
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                                                                                                                                                                                                                                                           SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD
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ilarity 100.0%;
Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       They are produced by removal of transit peptides from the precursor proteins (AAW15407-08). The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAT64529-30). AAT64547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterothexamers having alpha and beta subunite can be expressed that have higher aminating:deaminating activity ratios (i.e. higher capacity for glutamate synthesis) than homohexamers. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an ammonium-inducible, chloroplast-localised hexameric NADP-specific glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(8), useful to modulate nitrogen metabolism plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 44-46; 61pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmidt
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GLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV 520
                                                             CATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
                                                                                                                            SQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFF
                                                                                                                                                                                               SETRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGATVLSLSD
                                                                                                                                                                                                                                                              MRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
                                                                                                                                                                                                                                                                                                                             YSSAIGPYKGGLREHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEV
                                                                                                                                                                                                                                                                                                                                                                         QEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ 100
                                                                                                                                                                            SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD
                                                                                                                                                                                                                                           MRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
                                                                                                                                                                                                                                                                                                          YSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEV
                                                                                                           SQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP
                                                                                                                                                                                                                                                                                                                                                                                                                                        AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ
                                          CATQUEIDEQDAELLIKHGCQYVVEGANMPSTNEAIHKYNKÄGIIYCPGKAANAGGVAVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2500; DB 2;
Pred. No. 1.2e-229;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 487;
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MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV 110

MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV

AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170

120

60

AVSLÓPVFEKRÞELLÞÍFKQÍVEÞERVÍTFRVSWLDDAGNLÓVNRGFRVQYSSAÍGÞYKG GLRFHÞSVNLSIMKFLAFEQIFKNSLTTLÞMGGGKGGSDÞDÞKGKSDAEVMRFCQSFMTE

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RESULT 10
AAW15412
ID AAW15
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Query Match
Best Local S
Matches 476
                                                                                                                                                                              2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an ammonium-inducible, chloroplast-localised hexameric NADP-specific glutamate dehydrogenase (NADP-CDH) isoenzymes of Chlorella sorokiniana. They are produced by removal of transit peptides from the precursor proteins (AAW15407-08). The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAT64529-30, AAT64547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher aminating deaminating activity ratios (i.e. higher capacity for glutamate synthesis) than homohexamers. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                             Sequence 476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism; chloroplast; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW15412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 48-50; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT64548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-226226/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmidt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NADP-specific glutamate dehydrogenase beta subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2003
10-JUL-1997
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                             Similarity
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90.6%; ilarity 100.0%; Conservative
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                          Score 2465; DB 2; pred. No. 2.7e-226;
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                        The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutante dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonitoxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana mature NADP-glutamate dehydrogenase beta subunit, used in the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; nitrogen metabolism; plant; ammonium assimilation; transgenic; ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-499691/53.
N-PSDB; ABK51026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 31-32; 35pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SCHM/)
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Best Local
 with increased yield and
                                    WPI; 2004-533134/51.
N-PSDB; ADQ36730.
                                                                                                                                                                                                                                                          Nitrogen metabolism; plant; beta subunit; NADP-specific
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                                                                                                                                                                                                                                                                                                Mature NADP-specific GDH beta subunit,
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                                                                                                                                                                                                                                                                                                                                                                      standard; protein;
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nitrogen metabolism in plant cells, improved tolerance to ammonia toxic:
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                                                                                                                                                                                                                                                           glutamate dehydrogenase; GDH;
GDH; NADP-specific glutamate c
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Pred. No. :
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 cells, for plant toxicity and
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                                                                                                                                                                       ABU38763 standard;
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Pseudomonas aeruginosa.
                                Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                   19-JUN-2003
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                                                                encoded by Prokaryotic essential gene #24290
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                                                                                                                                                                                                                                                                                LNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 526
                                                                                                                                                                                                                                                                                                                                                DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                                                                                                                                                                                                                                                                                                 FTREQLQAVQDMKKKONSARISEYKSDTAVYVGDRRKFWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQRHISYVQDVÞAGDIGVGAREIGYLFGQYKRITKNYTGVLTÞKGQEYGGSEIRÞEATGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVSLOPVFEKRPELLPIFKQIVEPERVITERVSWLDDAGNLQVNRGFRVQYSSAIGPYKG
                                                                                                                                                                                                                                                                                                                                                                                              FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE
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                                                                                                                                                                                                                                                        LNWTREEVROKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
                                                                                                                                                                                                                                                                                                                            DAELLI KHGCQYVVEGANMPSTNEA I HKYNKAGI I YCPGKAANAGGVAVSGLEMTQNRMS
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                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by transforming plant cell with nucleic acid having
                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.6%; Score 2465; DB 8;
100.0%; Pred. No. 2.7e-226;
                                                                                                                                                                       445
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144

WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG 203

WVDDQGRVRVNRGYRVQMSSAIGPYKGGLRFHPSVNLGVLKFLAFEQVFKNSLTTLPMGG

124

VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS

VDAFLERLKRRDPDOPEFHOAVEEVLRSLWPFLEANPHYLEAGIIERIVEPERAILFRVP 64

吊 8

Query Match Best Local Similarity Matches 263; Conserv

Conservative

55;

48.1%;

Score 1309; DB 6; Pred. No. 9.3e-116; Mismatches 120;

Length 445; Indels

6

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of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid.

(2) an obst cell containing the vector; (3) an isolated concluded are:

(3) an isolated concluded to the nucleic acid.

(4) an antibed by the antisense conclude; (5) producing the polypeptide or its fragment whose expression is inhibited by the antisense collect acid; (4) an antibody capable of specifically binding colludar proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of identifying a gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation; (8) compound's activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (13) and inhibits the conduct is overexpressed or underexpressed; (13) determining the extent conduct is overexpressed or underexpressed; (13) and inhibits the conduct is overexpressed or unde
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
Wall
Sequence 445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 66687; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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                                                                         ftp.wipo.int/pub/published_pct_sequences
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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Carr G
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Forsyth
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Xu HH;
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                                                                                                                           The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis at therapy of pathological conditions, as molecular targets for diagnostic prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant
including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-1998;
27-JUL-1998;
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                                                               15-NOV-2002;
27-MAR-2003;
                                                                                                                                                                                                                   outer-membrane vesicle; antibacterial; antiinflammatory; meningococcal protein trafficking; localisation; infection;
                                                                                                                                                                                                                                                                                   26-AUG-2004
                                                                                                                                                                                                                                                                                                                                    ADP08330
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                                                                                                     17-NOV-2003; 2003WO-IB006281
                                                                                                                               03-JUN-2004
                                                                                                                                                        WO2004046177-A2
                                                                                                                                                                              Neisseria meningitidis
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Best Local Similarity
Matches 257; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New compositions having outer-membrane vesicles and proteins from Neissearia meningitidis, useful in the field of meningococcal biochemistry, in particular for preventing and/or treating meningococcal
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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        Issued_Patents AA:*

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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Maximum Match 100%
Listing first 45 summaries
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	991, Apr	122, App	2, Appli	2, Appli	21, Appl	17482, F	7623, A	7622, Ap	832, App	23, Appl	1153, Ap	20, Appl	22, Appl	13935,	6130, Ap	2, Appl:	12638, 7	

ALIGNMENTS

RESULT 1

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ATTORNEY/AGEN INFORMATION:
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
REFERENCE/OFKETON INFORMATION: (904) 375-8800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
TYPE: amino acid
TOPOLOGY: linear
TOPOLOGY: linear
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Matches 526; Conserv
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Patent No. 587994
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
ITILE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLECTIDES
TITLE OF INVENTION: NELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainswille
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                         1 MQTALVAKPIVAAPLAARPRCLAPWPCAWVRSAKRDVRAKAVSLEEQISAMDATTGDPTA
MQTALVAKPIVAAPLAARPRCLAPWPCAWVRSAKRDVRAKAVSLEEQISAMDATTGDFTA
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                                                                                           100.0%; Score 2720; DB 2; ilarity 100.0%; Pred. No. 7.6e-243; Conservative 0; Mismatches 0;
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Indels Length

Gaps

0

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526; 0

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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAC: (904) 372-8000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08828451 Patent No. 5985634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Schmidt, Philip

APPLICANT: Miller, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLU

TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/828,451
                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: ADDRESSEE: Saliwanch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2421 N.W.
CITY: Gainesville
STATE: Florida
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2421 N.W. 41st Street, Suite
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US-08-541-033A-4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
:-08-828-451-2
                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: MUST POLYPEPTIDES
TITLE OF INVENTION: RELATING TO THE '-
TITLE OF INVENTION: DEHYDROGENASES AND
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                  ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite CITY: Gainesville STATE: Florida
                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                COUNTRY: USA
ZIP: 32606
   CLASSIFICATION:
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100.0%; Pred. No. 7.6e-243;
rative 0; Mismatches 0;
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                                   US/08/541,033A
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AND -SUBUNITS OF G
METHODS OF USE
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RESULT 4
US-08-828-451-4
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APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAN
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
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Best Local S
Matches 512
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Patent No. 5985634
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: UFJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 375-8100
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Local Similarity 97.3%; Pred. No. 1.1e-233;
hes 512; Conservative 0; Mismatches 0; Indels 1
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TYPE: amino acid
TOPOLOGY: linear
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ER: UF155
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Best Local Similarity 97.3%;
Matches 512; Conservative
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INFORMATION FOR SEQ ID NO:
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPAX: (904) 375-8100
TELEPAX: (904) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
FILING DATE:
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467
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                                                                                                                                                                                                                                                                                                                      RPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNL 180
                    KLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
                                                                                                                                            DMKKKNNSARISEYKSDTAVYVGDRRKFWELDCQVDIAFFCATQNEIDEHDAELLIKHGC
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                                                            QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD 480
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Pred. No. 1.1e-233;
0; Mismatches 0;
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US-08-541-033A-24 ; Sequence 24, Application US/08541033A ; Patent No. 5879941

RESULT 5

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US-08-541-033A-24
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ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2421
STREET: Gainesville
CITY: Gainesville
cTATE: Florida
rca
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APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GITTLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/541,033A FILING DATE:
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                       GLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV
                                                                                        CATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
                                                                                                                    CATQNEIDEHDAELLI KHGCQYVVEGANMPSTNEAIHKYNKAGI I YCPGKAANAGGVAVS
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GLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV
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100.0%; Pred. No. 2.8e-223;
tive 0; Mismatches 0;
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APPLICANT: Schnidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND PO
TITLE OF INVENTION: RELATING TO THE - AND -S
TITLE OF INVENTION: DEHYDROGENASES AND METHOD
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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COMPUTER READABLE FORM:
MEDIUM YYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: UF TELECOMMUNICATION INFORMATION: TELEPHONE: (904) 375-8100
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                       MRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
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US-08-541-033A-26
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Best Local Similarity
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Patent No. 5
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APPLICANT: Miller, Philip
TITLE OF INVENTION: RELATIN
TITLE OF INVENTION: DEHYDRO
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             TELEFAX: (904) 372-580
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acid
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                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
                                                                                                                                                                                                                                                                                                                                                                    NAME: Whitlock, Ted W.
REGISTATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2421 N.W. CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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                                                                         MDATTGDFTALQKAVKQMATKAGTEGLVHG1KNPDVRQLLTE1FMKDPEQQEFMQAVREV
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AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG
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                                                                                                                                                                                                                                                                                               476 amino acida
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                              90.6%; Score 2465; DB 2; ilarity 100.0%; Pred. No. 2.6e-219; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                   (904) 372-5800
                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435
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RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
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                                                                                                                                                                                                                                                                                                                                                                                                       36,965
BER: UF155
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                                                                                                                                                                                 Length 476;
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; MOLECULE TYPE: protein US-08-828-451-26
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US-08-828-451-26
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Query Match 90.6%; Score 2465; DB 2; Best Local Similarity 100.0%; Pred. No. 2.6e-219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLECTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                   TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                    NAME: Whitlock, Ted W.
REGISTION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPACTION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                    TYPE: amino acid
TOPOLOGY: linear
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21 N.W. 41st Street, Suite A-1
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                  Length 476;
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Matches 476;

Conservative

0; Mismatches

Indels

0

Gaps

0

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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO E
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/99/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20646
LENGTH: 450
TYPE: PRT
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US-09-252-991A-20646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20646, Appl. Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
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                                                          GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI
                                                                                                     WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG
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                                 GKGGSDFDPKGKSDAEVMRFCQSFMSELYRHVGADLDVPAGDIGVGAREIGYLFGQYKRL
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TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
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                                                                                                                                                                                                                                              48.1%; Score 1309; DB 4; 59.2%; Pred. No. 2.2e-112; tive 55; Mismatches 120;
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US-09-328-352-5725
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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: HAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5725
LENGTH: 467
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                IYDSAM--GPSRRYNVDLAAGANIAGFTKVADAVKAQG
                                                                                        MPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKD
                                                                                                                                                              ARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVVEGAN
                                                                                                                                                                                                                                   GKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNS
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IHANCVRYGTKEDGTVNYVDGANI AGFVKVADAMLAQG
                                                                     MPSTLEAVEHFIEAKILYAPGKASNAGGVATSGLEMSQNAIRLGWTHAEVDERLHAIMKD
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US-09-134-000C-3884
                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lynn Do
                                                                                                                                                             Sequence 4489, Appearent No. 669970
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SEQ ID NO 3884
LENGTH: 448
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Best Local (
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APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating
TITLE OF INVENTION: Photomoriae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
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CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
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SEQ ID NO 4489
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PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
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ORGANISM: Streptococcus pneumoniae
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                                                                                                                                                                                       HEGTVWTYAGNYDIALPCATQNEINGEAAKRLVAQGVICVSEGANMPSDLDAIKVYKENG
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KDYLAGANIAAFENVANAMIAQGIV 448
                                           -DLAAGANIAGFTKVADAVKAQGAV 526
                                                                                           ILYGPAKAANAGGVAVSALEMSQNSLRLSWTREEVDDRLKDIMTNIFNTAKTTSETYGLD
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RESULT 13

US-08-86-640-3

Sequence 3, Application US/08886640

Patent No. 5998700

Patent No. 5998700

APPLICANT: Lightfoot, David

APPLICANT: Lightfoot, Maria V

TITLE OF INVENTION: PLANTS CONTAINING THE 9dha GENE AND TITLE OF INVENTION: METHODS OF USE THEREOF NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS: ADDRESSE: Pillsbury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W. CITY: Washington COUNTRY: United States

COUNTRY: United States

COMPUTER READABLE FORM: REDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS Word CURRENT APPLICATION NUMBER: US/08/886,640
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FILING DATE: 01-JUL-137,
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,058
FILING DATE: 02-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: KOKULLS, PAUL K.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 81163/241766
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-861-3503
TELEFAX: (202)-861-3503
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US-08-884-235-11
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Best Local S
Matches 241
                                                                                                                                                                                                                              Sequence 11, Application US/08884235 Patent No. 6329573
                                                                                                                                                                                                             GENERAL INFORMATION:
                             APPLICANT: Lightfoot, David A.
APPLICANT: Long, Lynn M.
APPLICANT: Long, Lynn M.
APPLICANT: Lightfoot, Maria E. Vidal
TITLE OF INVENTION: PLANTS CONTAINING THE gdhA GENE AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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nes 241; Conserv
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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
  ADDRESSEE: Pillsbury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W. CITY: Washington
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Patent No. 5573945
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APPLICANT: MATSUI, KAZUHIKO
APPLICANT: KURAHASHI, KAZUHIKO
TITLE OF INVENTION: MUTANT AND MI
TITLE OF INVENTION: L-GLUTAMIC AC
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLI
ADDRESSEE: P.C.
                                                                                                                       GENERAL INFORMATION:

APPLICANT: ONO, EIJI

APPLICANT: TSUJIMOTO, NOBUHARU

APPLICANT: MATSUI, KAZUHIKO

APPLICANT: KURAHASHI, KAZUHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 residues
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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COUNTRY: United States of America
CIP: 20005-3918
ZIP: 20005-3918
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SYSTEM: PC-DOS/MS-DOS
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                       MCCLELLAND, MAIER & NEUSTADT
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Length 447; Indels

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Search completed: July 9, 2005, 18:36:41 Job time: 45 secs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 54.0
Matches 241; Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,193A
FILING DATE: 09-0AN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-714-0
TELEPAN: 703-413-300
TELEPAN: 703-413-300
TELEPAN: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: USA
COUNTRY: USA
COUNTRY: 22202
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: FC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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CITY: A
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                                                                                                                                                                                                                                                                 306 EGQQPWSL--PVDIALPCATQNELDVDAAHQLIANGVKAVAEGANMPTTIEATELFQQAG 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 447;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 200000000
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2720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep:*
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1224.155 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1294.5	1297.5	1309	2465	2465	2508	2508	2621	2621	2720	2720	Score
47.6	47.7	48.1	90.6	90.6	92.2	92.2	96.4	96.4	100.0	100.0	Query Match
444	444	445	476	476	487	487	512	512	526	526	Query Match Length DB
15	15	15	16	9	16	9	16	9	16	9	: B
US-10-282-122A-66041	US-10-282-122A-65129	US-10-282-122A-66687	US-10-627-886-26	US-09-070-844-26	US-10-627-886-24	US-09-070-844-24	US-10-627-886-4	US-09-070-844-4	US-10-627-886-2	US-09-070-844-2	ID
	Sequence 65129, A	Sequence 66687, A	Sequence 26, Appl	Sequence 26, Appl	Sequence 24, Appl	Sequence 24, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Description

45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	7.4
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-10-282-122A-587	-10-282-122A-7828	-10-282-122A-5564	-10-282-122A-6287	-282-122A-6862	-10-282-122A-727	-10-369-493-29	10-282-122A-6081	-10-282-122A	-10-282-122A-5399	738-626-6	-10-282-122A-	-10-369-493-1	-10-369-493-8	-10-425-114-7	-10-282-	0-282-122A-4328	-10-36	-10-282-122A	-10-369-493-6	-282-122A-51	-10-369-493-1728	-10-472-928-2	-10-282-122A-7402	-10-282-122A-	-10-282-122A-7232	-10-282-122A-5809	-10-260-877-9	-10-282-122A-5731	0-282-122A-4	69-493-983	-10-369-493-1394	-10-282-122A-	
e 58700,	ce 78288,	ce 55644,	ce 62874,	ce 68627,	ce 72769,	8	e 60810,	ce 75593,	ce 53998,	6982,	equence 60243,	equence 10621,	equence 8215	equence 72961,	equence 52117,	e 43284,	equence 859, Ap	e 48442,	equence 617, A	51278,	17284,		74024,	66870,	72329,	58096,	90, Ap	57310,	9 45200,	9839,	13947,	€ 6753	Cdronor Total

ALIGNMENTS

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                        Sequence 2, Application US/10627886 Publication No. US20040128710A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                   NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik &
STREET: 2421 N.W. 41st SI
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                    APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBUNITS OF GI
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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Pred. No. 5.7e-236;
                                                                                               & Saliwanchik
Street, Suite A-1
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  Sequence 4, Application US/09070844
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US-10-627-886-2
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Best Local Simi
Matches 526;
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TELEPAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 09/070,844

FILING DATE: 01-MAY-98

APPLICATION NUMBER: 08/725,596

APPLICATION NUMBER: 08/541,033

FILING DATE: 08-00T-95

ATTORNEY/AGENT INFORMATION:

NAME: L10yd, Jeff

REGISTRATION NUMBER: 35,589

REFERENCE/DOCKET NUMBER: UF-155CD3

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/10/627,886
FILING DATE: 24-Uul-2003
CLASSIFICATION: <Unknown>
                                    481
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                                                                                                 QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD
                                                                                                                                                                             DMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNL
KLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
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                                                                            QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD
                                                                                                                                                       DMKKKNINSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGC
                                                                                                                                                                                                                                    XDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ
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SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE:
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 96.4%;
Local Similarity 97.3%;
es 512; Conservative
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                                                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                  181
                                361
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                                                                                                                                                                        241 VPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVL 300
                                                                                                                                                                                                                                                                                                      107 RPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNL 166
                                                                                                                                                                                                                                                                                                                            121 RPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNL 180
347
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                DMKKKANISARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGC 420
                                                                                                                                                                                                                                                  SIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVWRFCQSFMTELQRHISYVQD 240
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                                                                                              KDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ 360
                                                                                                                                                                                                                          SIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVNRFCQSFMTELQRHISYVQD
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                                                                      KDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ 346
                                                                                                                                                  VPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVL
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(904) 372-5800
OR SEQ ID NO: 4:
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Pred. No. 4.6e-227;
0; Mismatches 0;
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US-10-627-886-4
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Publication No. US20040128710A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R
Miller, Philip
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (352) 375-810
TELEPAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Ver
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAX-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
APPLICATION NUMBER: 08/541,033
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBUNITS OF G:
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                               Similarity
                                                                   LQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEK 120
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RPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNL
                                                                                                                           MQTALVAKPIVA------CAWVRSAKRDVRAKAVSLEEQISAMDATTGDFTA
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STATE: Florida
COUNTRY: USA
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                                           LQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEK 106
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                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 512 amino acids
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                             96.4%;
97.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375-8100
                                                                                                                                                                                                             0;
                                                                                                                                                                                                           Score 2621; DB 16;
Pred. No. 4.6e-227;
0; Mismatches 0;
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                                                                                                                                                                                                             Indels
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; INFORMATION FOR SEQ ID NO: 24
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-844-24
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US-09-070-844-24
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Patent No. US20020062495A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,84
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (904) 375-8100
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
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APPLICATION NUMBER:
FILING DATE:
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                                                                                                       TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                        ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                    : (904)
(904) 372-5800
TD NO: 24:
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                                                                                                                                                                                                                                                                                                                   Version
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RESULT 6
US-10-627-886-24
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Best Local Similarity
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Uul-2003
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
CORDENCE ADDRESSE: SAliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schmidt, Robert R.

Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBNITS OF GI
DEHYDROGENASES AND METHODS OF USE
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STATE: Florida
COUNTRY: USA
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Pred. No. 6.6e-217
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RESULT 7
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                                                                                                                                                             Sequence 26, Application US/09070844
Patent No. US20020062495A1
GENERAL INFORMATION:
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Best Local
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SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                      APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: ROUGEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 92.2%; Score 2508; DB 16; Length Local Similarity 100.0%; Pred. No. 6.6e-217; hes 486; Conservative 0; Mismatches 0; Indels
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REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            482
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 476 amino acids TYPE: amino acid TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                                                                                     GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCABLLLEKGAIVLSLSDSQGYVYBPNG
                                                                                                                                                                                                                                                                LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQBYGGSEIRPBATGY
                                                                                                                                                                                                                                                                                                                               GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE
                                                                                                                                         FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKFWELDCQVDIAFPCATQNEIDEH
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                                                                                                                        FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
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(904) 372-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.6%; Score 2465; DB 9; 100.0%; Pred. No. 4.8e-213; tive 0; Mismatches 0;
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US-10-627-886-26; Application US/10627886; Sequence 26; Application US/10627886; Publication No. US20040128710A1; GENERAL INFORMATION:

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US-10-627-886-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
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Miller, Philip
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                     FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                              GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                   GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                             LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
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FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 2421 N.W. CITY: Gainesville
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100.0%; Pred. No.
-ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2465; DB 16;
Pred. No. 4.8e-213;
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                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas aeruginosa US-10-282-122A-66687
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PRIOR FILLING DATE: 2000-03-21
PRIOR PELLORITION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR PELLORITION NUMBER: 60/207,727
PRIOR PELLORITION NUMBER: 60/207,335
PRIOR PELLORITION NUMBER: 60/230,335
PRIOR PELLORITION NUMBER: 60/230,335
PRIOR PELLORITION NUMBER: 60/230,347
PRIOR PELLORITION NUMBER: 60/230,347
PRIOR PELLORITION NUMBER: 60/230,347
PRIOR PELLORITION NUMBER: 60/230,347
PRIOR PELLORITION NUMBER: 60/230,347
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PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
SOPTWARE: Patentin version 3.1
SEQ ID NO 66687
LENGTH: 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                  263;
                                                                                                                                                                                        86 VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS 143
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GKGGSDFDFKGKSDAEVMRFCQSFMTELQRHISYVQDVFAGDIGVGAREIGYLFGQYKRI
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                                                                    WVDDQGRVRVNRGYRVQMSSAIGPYKGGLRFHPSVNLGVLKFLAFEQVFKNSLTTLPMGG
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Carr, Grant
Carroto, Robert
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Zyskind, Judith
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Malone, Cheryl
Haselbeck, Robert
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Forsyth, R.
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; Pred. No. 7.3e-109;
55; Mismatches 120;
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; ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65129
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                                                          Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 786.4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 65129, Application US/10282122A
Publication No. US20040029129A1
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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                             LENGTH: 44
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes
                                                                                                                                                                                                                                                                                                           OR FILING DATE: 2000-03-21

OR APPLICATION NUMBER: 60/206,848

OR FILING DATE: 2000-05-23

OR APPLICATION NUMBER: 60/207,727

OR FILING DATE: 2000-05-26

OR APPLICATION NUMBER: 60/230,335

OR APPLICATION NUMBER: 60/230,335

OR FILING DATE: 2000-09-06
                                                                                                                       FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
                                                                                                                                                                                     APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
                                                                                                                                                                     APPLICATION NUMBER: 60/267,636
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: Zamudio, Carlos
: Malone, Cheryl
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Trawick, John
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Ohlsen, Kari
Zyskind, Judith
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dio, Carlos
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US-10-282-122A-66041
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
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PRIOR PELING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/230,335
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PRIOR PELICATION NUMBER: 60/230,3625
PRIOR PELICATION NUMBER: 60/253,625
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PRIOR PELICATION NUMBER: 60/253,625
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Best Local Similarity
Matches 257; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential FILE REFERENCE: ELITA, 034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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Forsyth, R.
Xu, H.
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Zyskind, Judith
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Malone, Cheryl
Haselbeck, Robert
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dio, Carlos
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Sequence 152, Application US/10275026A

Publication No. US20040087770A1

GENERAL INFORMATION:
APPLICANT: Tang, Christoph
TITLE OF INVENTION: Virulence Genes, Proteins, and FILE REFERENCE: GJE-6436

CURRENT APPLICATION NUMBER: US/10/275,026A

CURRENT FILING DATE: 2003-10-31

PRIOR FILING DATE: 2001-05-08

PRIOR FILING DATE: 2001-05-08

PRIOR FILING DATE: 2000-05-08

S-10-275-026A-152
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                    TYPE: PRT ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 444
TYPE: PRT
ORGANISM: Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKR
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TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,337
PRIOR PILLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
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OR PILING DATE: 2000-99-06
OR FILING DATE: 2000-99-06
OR PILING DATE: 2000-99-09
OR APPLICATION NUMBER: 60/230,347
OR FILING DATE: 2000-99-09
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
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Zamudio, caryl
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Carr, Grant
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto, R
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trawick, John
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57.1%; Pred. No. 1.5e
tive 72; Mismatches
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l.5e-107;
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GENERAL INFORMATION: OF APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR APPLICATION NUMBER: US/10/369,493
UNDBER OF SEQ ID NOS: 47374
SEQ ID NO 13947
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-10-369-493-13947
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US-10-282-122A-67538
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                         LENGTH: 445
TYPE: PRT
ORGANISM: Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGQTPWSLPC--DIALPCATQNELGAEDARTLLRNGCICVAEGANMPTTLEAVDIFLDAG 364
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                                                                                                                                                                                                           ; LENGTH: 454
TYPB: PRT
; ORGANISM: Desulfitobacterium hafniense
US-10-369-493-9839
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                                                                                                                                                                                                                                                                                   APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9839
                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
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                                                                                                                                   Matches
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Best Local Similarity
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144 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLREHPSVNLSIMKFLAFEQIFKNSLTTLPMGG
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                                                                                       VRQLLTEIEMKDPEQQEFMQAVREVAVSLQPVFEKRPEL--LPIFKQIVEPERVITFRVS 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WVDDQGRVQVNRGFRIQMNSAIGPYKGGLRFHPSVNLGVLKFLAFEQTFKNSLTSLPMGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG
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                                                   VQEVLEQAVKRNPGEABFHQALREVLESLEPVLEKRPDLKEAGILERIVEPERQILFRVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKGGSDFDPKGKSDAEVMRFCQAFMSELYRHIGADVDVPAGDIGVGAREIGFLFGQYKRL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VESFLARLKKRDPDQPEFHQAVEEVLRSLWPFLEANPHYLTSGILERICEPERAVVFRVS
                                                                                                                                   Conservative
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                                                                                                                               ; Score 1259; DB 15;
; Pred. No. 2.4e-104;
68; Mismatches 112;
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GGTVVA GGTVVA ELDCQV :	TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY 323
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	EYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLV

Search completed: July 9, 2005, 18:39:34 Job time : 168 secs

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ALIGNMENTS

glutamate dehydrogenase (NADP) (EC 1.4.1.4) precursor - Chlorella sorokiniana (fragment) N;Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase C;Species: Chlorella Sorokiniana (fragment) C;Date: 30-Jun-1921 #sequence revision 23-Mar-1995 #text_change 09-Jul-2004 C;Accession: S17949; S17950; S19030 R;Cock, J.M.; Kim, K.D.; Miller, P.W.; Hutson, R.G.; Schmidt, R.R. Plant Mol. Biol. 17, 1023-1044, 191 Plant Mol. Biol. 17, 1023-1044, 191 A;Title: A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP A;Reference number: S17949; MUID:92032762; PMID:1718478 A;Genome: nuclear
A;Introns: 6/2; 29/1; 40/3; 56/3; 85/3; 127/3; 149/3; 175/1; 183/3; 211/1; 246/1; 272/2;
A;Introns: 6/2; 29/1; 40/3; 56/3; 85/3; 127/3; 149/3; 175/1; 183/3; 211/1; 246/1; 272/2;
C;Superfamily: glutamate dehydrogenase (NADP; oxidoreductase
C;Keywords: chloroplast; hexamer; NADP; oxidoreductase
F;202/Binding site: substrate (Lys) #status predicted S 밁 S . 명 Ś 밁 Ś A; Molecule type: DNA A; Residues: 1-219, 'LW', 222-523 <SCH> A; Cross-references: EMBL: X58831 A; Accession: S19030 submitted to the EMBL Data Library, April 1991
A;Reference number: S19030 A;Cross-references: EMBL:X58832; NID:g18272; PIDN:CAA41636.1; PID:g18273 A;Molecule type: mRNA A;Residues: 1-523 <COC2> A;Molecule type: DNA A;Residues: 1-523 <COC> A; Accession: S17950 A;Cross-references: UNIPROT:P28998; EMBL:X58831 ;Genetics: Matches Query Match Best Local Similarity 194 197 134 137 VITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSL 196 74 77 19 17 488; LVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPER 136 ARPRCLAPWPCAWVRSAKRDVRAKAVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEG TTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYL 256 VITERVSWLDDAGNLQVNRGERVQYSSAIGPYKGGLREHPSVNLSIMKELAFEQIEKNSL LVHGIKNPELRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPER 133 ALPRAVA---CARGRSAKRDVAAK--RLRSRSPRMDATTGDFTALQKAVKQMATKAGTEG TTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYL Conservative 91.5%; Score 2488.5; Pred. No. 3.2e 4; Mismatches 4; .5; DB 1; 3.2e-175; Indels Length . 523; 5. Gaps 193 73

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glutamate dehydrogenase (NADP) (EC 1.4.1.4)

N;Alternate names: glutamic dehydrogenase; N
C;Species: Giardia lamblia
C;Date: 31-Dec-1993 #sequence_revision 23-Ma
C;Accession: A42489
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C;Keywords: NADF; oxidoreductase
F;125/Binding site: substrate (Lys) #status predicted
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J. Biol. Chem. 267, 7539-7544, 1992
J. Biol. Chem. 267, 7539-7544, 1992
A;Title: Isolation and characterization of A;Reference number: A42489; MUID:92218410;
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                        AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYN
                                                                                                                                          EKLIQLGAKYLTFSDSNGTIVDKDGFNEEKLAHLMYLKNEKR-GRVSEFKDKYPSVAYYE
                                                                                                                                                                                                                 EFTGVLTGKNVXWGGSFIRPEATGYGAVYFLEEMCKDNNTVIRGKNVLLSGSGNVAQFAC
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                                                                       G--KKPWECFEGQMDCIMPCATQNEVSGDDATRLVGLGLKFVAEGANMPSTAEAVHVYHA
                                                                                               GDRRKPWE-LDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANWPSTNEAIHKYNK
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KGVMYGPAKASNAGGVSVSGLEMSONSVRLQWTAEEVDQKLRGIMRGIFVACRDTAKKYG
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Pred. No. 1.2e-89;
77; Mismatches 111;
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PMID:1559991
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NCBIP:94074)
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glutamate dehydrogenase PA4588 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C;Accession: H83072 R;Stover, C:K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, i. Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: H83072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source:
C; Genetics:
A; Gene: gdhA; PA4588
C; Superfamily: glutamat
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A; Residues: 1-445 <STO>
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                                                                                                                                                            DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG
                                                                                                                                                                                                                              CAELLLEKGAIVLSLSDSQGYVYBPNGFTREQLQAVQDMKKKNNSARISBYKSDTAVYVG
                                                                                                                                                                                                                                                                                                                                                    GKGGSDFDPKGKSDAEVMRFCQSFMSELYRHVGADLDVPAGDIGVGAREIGYLFGQYKRL
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NYVKGANIAGEVKVADAMLAQGVV
                                DLAAGANIAGETKVADAVKAQGAV
                                                                     ILYAPGKASNAGGVAVSGLEMSQNAMRLRWSEGEVDTKLHGIMQSIHHACLLYGEEQGRV
                                                                                       IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSA-MGPSRRYNV
                                                                                                                                                                                                           AARKVMEMGGKVISLSDSEGTLYAEAGLSDEQWEYLMELKNVRR-GRIREMAEQFSLQFL
                                                                                                                                                                                                                                                                                 SNOFTSVLTGKGLSYGGSLIRPEATGFGCVYFAQEMLKDRGRGFDGQRVAISGSGNVAQY
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Pred. No. 1.6e-88;
5; Mismatches 120
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K., Lim,
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glutamate dehydrogenase, NADD-specific NMB1710 [imported] - Neisseria mening C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: H81050 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Doug

meningitidis

(stra)

K.E.; Eisen, Dougherty, B

J.A.

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A;Residues: 1-444 <PAR>
A;Cross-references: UNIPROT:Q9JT56;
A;Experimental source: serogroup A,
C;Genetics: A;Gene: gdhA; NMA1964
C;Superfamily: glutamate dehydrogena
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                             Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall Nature 404, S02-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B81825
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glutamate dehydrogenase (NADP) (EC 1.4.1.4) NMA1964 [imported] - C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change (C;Accession: B81825 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher (Horoyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Control (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (Marcher) (March
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A;Cross-references: UNIPROT:Q9JY71; GB:AE002521;
A:Fxnerimental source: serogroup B, strain MC58
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A;Molecule type: DNA
A;Residues: 1-444 <TET>
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Science 287, 1809-1815,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.; Gill, J.; Scarlato,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72; Mismatches 104;
                                                                                                                                                      GB:AL162757; GB:AL157959; NID:g7380371; strain Z2491
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M.A.;
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                                                                         AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY-
                                                                                                                     YFENOKPWGV--AABIALPCATONELDEEAAKTLLANGCYVVAEGANMPSTLGAVEOFIK
                                                                                                                                     VGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 441
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                                                         AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTREEVDQRLFGIMQSIHESCL----KYG
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C;Accession: Ã64053
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, R;Fleischmann, R.D.; Scott, J.; Shirley, R., Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800 A;Status: nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-449 <TIGP>
A;Cross-references: UNIPROT: P43793; GB: U32704; GB: L4202 C;Superfamily: glutamate dehydrogenase (NAD(P)+) C;Keywords: NADP; oxidoreductase glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Haemophilus influenzae C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #rawr on T. A; Accession: A64053 ;Species: Haemophilus influenzae ;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 GB:L42023; NID:g1573143; not shown (strain PIDN: AAC21858.1; Вd KW20)

4 >

ᅜ δ 밁 ð Query Match Best Local : Local Similarity 247; 11 90 SDFDFKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNY AGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGG LTKVAQRDGYQPEFLQAVREVFTSIWPFLEANPKYRSEALLERLVEPERAFQFRVAWTDD LTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRVSWLDD Conservative 45.5%; 55.6%; ; Score 1238; DB 2; ; Pred. No. 2.8e-83; 64; Mismatches 117 Length 449; Indels 16; Gaps 130 207 70 ທ

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RESULT 7
T10487
T10487
Glutamate dehydrogenase (NADP) (EC 1.4.1.4) -
C;Species: Prevotella ruminicola
C;Species: 16-U11-1999 #sequence_revision 16-Jul-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T10487
R;Wen, Z.T.; Morrison, M.
submitted to the EMBL Data
A;Reference number: Z17049
A;Accession: T10487
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C;Superfamily: glutamate dehydrogenase
C;Keywords: NADP; oxidoreductase
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A; Residues: 1-444 <WEN>
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Matches 242
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                                                                                                                                                                     ELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDR
                                                                                                                                                                                                                                                  NYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCA
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YCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAM--GPSRRYNVD
                                                              ARPW--GEKADIATPCATQDEINEAEAKTLIANGVFAVSEGANMPTEPAAIKVFQDAKIL
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NADP-specific glutamate dehydrogenase [imported] - Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004 C;Accession: H95151

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RESULT H95151

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RESULT 8

D98019

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G1 transte dehydrogenase (NADP) (EC 1.4.1.4) [imported] - Streptococcus pneumoniae c;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C;Accession: D98019

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhrz, P.; Sun, P.M.; Minkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Atthors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskuns A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Recession: D98019

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 <KUR>
A;Residues: 1-448 <KUR>
A;Residues: 1-448 <KUR>
A;Residues: Linteror. Order GB.AERO07317. DIDN.AAK99984 1: DID:G15458811.
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YVKGANVAGFMKVAKAMMAQG
                                                                                                         IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNV-
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KDYLAGANIAAFENVANAMIAQGIV
                                                                           IFYGPAKAANAGGVAVSALEMSQNSLRLSWTREEVDGRLKDIMTNI FNTAKTTSETYGLD
                                                                                                                                                     HEGSVWTYAGNYDIALPCATQNEINGEAAKRLVAQGVICVSEGANMPSNLDAIKVYKENG
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                       -DLAAGANIAGFTKVADAVKAQGAV
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, P.; McAhren,
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-458 <STO>
A;Cross-references: UNIPROT:Q9KB34; GI
A;Experimental source: strain C-125
C;Genetics:
A;Gene gdhA
C;Superfamily: glutamate dehydrogenase
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E83912
                                                                                                                                                         R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Mucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heicon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Recession: H95151

A;Status: preliminary
                                                                                                                                                                                                                                     NADP-specific glutamate dehydrogenase gdhA [imported] - Bacillus halodurans (strain C;Species: Bacillus halodurans C;Decies: Dacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: E83912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: >r1) C;Superfamily: glutamate
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A;Residues: 1-448 «KUR»
A;Cross-references: UNIPROT:Q97QB4;
A;Experimental source: strain TIGR4
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Best Local S
Matches 247
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   dehydrogenase (NAD(P)+)
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                                                                       GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05
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A;Residues: 1-424 <WHI>A;Cross-references: UNIPROT:Q9RTN9; GB:AE002013; GB:AE000513; NID:g6459484; PIDN:AAF1127:
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: E75362

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus A;Title: Genome sequence of the radioresistant bacterium Deinococcus A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glutamate dehydrogenase - Deinococcus radiodurans (C;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
E75362
                                                                                                                                                                                                                   A; Map position:
C; Superfamily: (
                                                                                                                                                                                                                                                       A;Gene: DR1718
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                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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488
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                                                                                                                                                                                                                     glutamate dehydrogenase
                                                                                                                                                 Conservative
                                                                                                                                             44.3%; Score 1205.5; DB 2; 56.2%; Pred. No. 6.3e-81; ative 61; Mismatches 119;
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Pred. No. 3e-81;
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T.; Zalewski,
                                                                                                                                               Gaps
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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A64936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 03-Aug-1984 #sequence_revision 20-Sep-1984 #text_change C;Accession: A00382; A22413; A64936 R;McPherson, M.J.; Wootton, J.C.
Nucleic Acids Res. 11, 5257-5266, 1983
A;Title: Complete nucleotide sequence of the Escherichia coli gd A;Reference number: A00382; MUID:83272967; PMID:6308576
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DEECEN
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                                                                                                                                                                A; Map position: 27 min C; Superfamily: glutamate dehydrogenase (NAD(P)+) C; Keywords: homohexamer; NADP; oxidoreductase
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A;Title: Complete nucleotide sequence of the glutamate dehydrogenase gene from Es A;Reference number: A22413; MUID:84209849; PMID:8373501
A;Accession: A22413; MUID:84209849; PMID:8373501
                                                                                                                                                                                                                                       A; Experimental source: C; Genetics:
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A; Residues: 1-447 < VAL>
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A; Residues: 1-447 < MCP>
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                                                                                                                                                                                                                        A;Gene: gdhA
                                                                                                                                                                                                                                                        A;Cross-references: GB:AE000271; GB:U00096; NID:g1788058; A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-447 <BLAT>
                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation
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                                     VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPEL--LPIFKQIVEPERVITFRVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEMSQNAQRLSWTREEVDQRLRSIMSAIHDSCLEYGRRPDRHVSYLDGANIAGFVKVATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRR--YNVDLAAGANIAGFTKVADA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATQNELGADDARTLIAGGVRVVAEGANMPCDLAAIQAFEEAGVLYAPGKATNAGGVATSG
     LESFLNHVQKRDPNQTEFAQAVREVMTTLWPFLEQNPKYRQMSLLERLVEPERVIQFRVV
                                                                          Conservative
                                                                                         44.2%;
                                                                                                                                              (Lys) #status predicted
                                                                          67;
                                                                        Pred. No. 1.5e-80; 7; Mismatches 128;
                                                                                             Score 1201; DB 1;
Pred. No. 1.5e-80;
                                                                                                          Length 447;
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A;Residues: 1-443 <KUR>
A;Residues: 1-443 <KUR>
A;Cross-references: UNIPROT:Q97L29; GB:AE001437; PIDN:AAK78713.1; PID:g15023619; GSPDB:GN
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
C;Genetics:
A;Gene: CAC0737
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, F.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADP-specific glutamate dehydrogenase [imported] - Clostridium acetobutylicum c;Species: Clostridium acetobutylicum C;Decies: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: F96990
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NVDLAAGANI AGETKVADAVKAQGAV
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                                                                                                                                                                                                                                                                                                                                                                 44.18;
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                                                                                                                                                                                                                                                                                                                                            Score 1199; Db 2,
Pred. No. 2e-80;
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444 IIYCPGKAANAGGVAVSGLEMTONRMSLNWTREEVRDKLERIMKDIYDSAM---GPSRRY 500
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                                                                                                                                                             DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG
                                                                                                                                                                                                                                                                               CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG
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VLFAPGKAANAGGVATSGLEMAQNAARLGWKAEKVDARLHHIMLDIHHACVEHGGEGEQT
                                                                                                                     EGQQPWSL--PVDIALPCATQNELDVDAAHQLIANGVKAVAEGANMPTTIEATELFQQAG
                                                                                                                                                                                                                                          AIEKAMEFGARVITASDSSGTVVDESGFTKEKLARLIEI-KASRDGRVADYAKEFGLVYL
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Markarova, K.S.; Smith, D.R. Zeng, 0 Gibson,

> æ : Lee,

Solvent-Producing Bacterium Clos

Length 443;

4 LKHVMDDVIKRNPNEPEFHOAVKEVLLSLEIVAEKHPEWVKDKIFDKIVEPERQIIFRVP GKGGSDFDFKGKSDAEVMRFCQSFMTELQRHISYVQDVFAGDIGVGAREIGYLFGQYKRI WVDDNGEEHINRGFRIQFNSAIGPYKGGLRFHPSVNLGIVKFLGFEQIFKNSLTGLPIGG WLDDAGNLQVNRGERVQYSSAIGPYKGGLREHPSVNLSIMKFLAFEQIFKNSLTTLPMGG RNESTGVLTGKGLTLGGSLVRTEATGYGLCYFMNEALKAKGKSFDGATVIISGSGNVAIY TKNYTGYLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY GKGGSDFNPKSKSNSEIKRFCQSFMLELNKYIGANTDVPAGDIGVGSREIGYLYGMFKKI Indels 12; Gaps 381 243 323 183 263 123 203 63

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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; I
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-447 <HAY>
A;Cross-references: UNIPROT:Q8XDW9; GB:BA000007; PIDN:BAB35890.1; PID:g13361934; GSPDB:
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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N--YVQGANIAGEVKVADAMLAQGVI 447
                                                                                               IIYCPGKAANAGGYAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAM----GPSRRY 500
                                                                                                                                                              DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG 443
                                                                                                                                                                                                                 AIEKAMEFGARVITASDSSGTVVDESGFTKEKLARLIEI-KSSRDGRVADYAKEFGLVYL 305
                                                                                                                                                                                                                                                    CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG
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                        NVDLAAGANIAGETKVADAVKAQGAV 526
                                                                                                                                             EGQQPWSV--PVDIALPCATQNELDVDAAHQLIANGVKAVAEGANMPTTIEATELFQQAG
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Search completed: July Job time : 43 secs

2005, 18:35:51

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A;Molecule type: DNA
A;Residues: 1-447 <STO>
A;Cross-references: UNIPROT:Q8XDW9; GB:AE005174;
A;Experimental source: strain O157:H7, substrain
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: gdhA
C;Superfamily: glutamate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: G85785
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
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                                                                       VLFAPGKAANAGGVATSGLEMAQNAARLGWKAEKVDARLHHIMLDIHHACVEHGGEGEQT
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                                                                                                                                                                                                                                                                                           SUNTACVFTGKGLSFGGSLIRPEATGYGLVYFTEAMLKRHGMGFEGMRVSVSGSGNVAQY
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EDL933
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Q7r3n7 giardia lan
P28724 giardia lan
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Q66183 uncultured
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Q6f467 acinetobac
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          Nature 419:498-511(2002).
EMBL; AE014820; AAN36899.
HSSP; P24295; IAUP.
GO; GO:0016491; F:oxidore
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InterPro; IPR006095; GLFV
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Eukaryota; Alveolata;
NCBI_TaxID=36329;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO:0006520; P:amino acid metabolism; IEA.
erPro; IPR006095; GLFV_dehydrog.
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Best Local S
Matches 267
                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2004
01-MAR-2004
01-MAR-2004
                                                                PubMed=12368855; DOI=10.1038/nature01099;
Carlton J.M., Angivoli S.V., Suh B.B., Kooij T.W., Pertea M., Salrton J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Popp M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoabib A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Valdya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7RQ39
Q7RQ39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006096; GLEV_dehydrog_C.
InterPro; IPR006097; GLEV_dehydrog_N.
Pfam; PF00208; GLEV_dehydrog; 1.
Pfam; PF02812; GLEV_dehydrog_N; 1.
PRINTS; PR00082; GLFDHDRGNASE; 1.
PROSITE; PR00074; GLEV_DEHYDROGENASE; 1.
PROSITE; PS00074; SLEY_DEHYDROGENASE; 1.
          Carucci D.J.;
"Genome sequence and comparative analysis parasite Plasmodium yoelii yoelii.";
                                                                                                                                                                                                                                                                          STRAIN=17XNL;
                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata; NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                         Plasmodium yoelii yoelii.
                                                                                                                                                                                                                                                                                                                                                                                                              Glutamate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                Name=PY01264;
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mes 267; Conserv
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                                                                                                                                                                                                                                                                                          FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITK
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Pred. No. 2e-8:
56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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annotation update)
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                                 model
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Koo H.L.,
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Best Local Simi
Matches 264;
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InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF03372; Exo endo phos; 1.
Pfam; PF00308; GLFV_dehydrog_N; 1.
Pfam; PF00208; GLFV_dehydrog_N; 1.
Pfam; PF002812; GLFV_dehydrog_N; 1.
PRINTS; PR000082; GLFDHDRRNASE
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
SEQUENCE 1203 AA; 133099 MM; DBE1988
                                                                                                                                  Q7YZU9;
Q7YZU9;
01-OCT-2003
01-OCT-2003
01-MAR-2004
STRAIN-ATCC 50380;
PubMed=12820901; DOI=10.1186/1471-2148-3-14;
Andersson J.O., Roger A.J.;
                                                                 Spironucleus barkhanus.
Eukaryota; Diplomonadida;
EUKBI_TaxID=103874;
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HSSP; P24295; 1AUP.
GO; GO:0016491; Froxidoreductase activity
GO; GO:0006520; P;amino acid metabolism;
                                                                                                                     Glutamate dehydrogenase
                                             SEQUENCE FROM N.A.
                                                                                                           Name=gdh;
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EMBL/GenBank/DDBJ whole
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54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFEGVLTGKNIKWGGSNIRSEATGYGVAYFAENALSDMNESLKNKTCIVSGSGNVAQYLV
                                                                                                                                                                                                                                                   TDLVAGANIAGFLKVADSFIEQGGL
                                                                                                                                                                                                                                                                                                    ILICPSKAANAGGVAVSGLEMSQNSMRLQWSSEETDQKLQKIMKNIYEQCCDASQKYTGE 1176
                                                                                                                     (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last seq
(TrEMBLrel. 26, Last ann
shydrogenase (Fragment).
                                                                                                                                                                                    PRELIMINARY;
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                                                                                  Hexamitidae;
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                                                                                                                                 Last sequence update)
Last annotation update)
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Pred. No. 5.5e-84;
5; Mismatches 108;
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abolism; IEA.
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Matches 262
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InterPro; IPR006096; GLFV_dehydrog.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF002812; GLFV_dehydrog_N; 1.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1
NON_TER

1 1 1
Morrison H.G., McArthur A.G., Adam R.D., Aley S. Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ da
-!- CAUTION: The sequence shown here is derived
EMBL/GenBank/DDBJ whole genome shotgun (WGS)
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EMBL; AF533884; AAR83851:1; -.

HSSP; P24295; IAUP.

GO; GO:001666
                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 20
GLP_39_39379_38030.
Giardia lamblia ATCC 5080:
Eukaryota; Diplomonadida;
                                                                                                                                       STRAIN-WB C6;
                                                                                                                                                                 SEQUENCE FROM N.A.
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01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                        Q7R3N7;
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                       k/DDBJ databases
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R EMBL; AACB0100002.,

R HSSP; P24295; IAUP.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

JR GO; GO:0006520; P:amino acid metabolism; IEA.

DR InterPro; IPR006095; GLFV_dehydrog_C.

DR InterPro; IPR006097; GLFV_dehydrog_N.

DR Pfam; PF00208; GLFV_dehydrog_N, 1.

DR Pfam; PF00208; GLFV_dehydrog_N; 1.

DR PFNNTS; PR00082; GLFV_dehydrog_N; 1.

DR PRINTS; PR00082; GLFV_DEHYDROGENASE; 1.

DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.

DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.

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P28724; Q24961;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence up
29-MAR-2004 (Rel. 43, Last annotation
NADP-specific glutamate dehydrogenase
                                                                                                                                                                                                                                              dependent glutamate dehydrogenase):
Giardia lamblia (Giardia intestinalis).
Eukaryota, Diplomonadida, Hexamitidae, Giardiinae,
NCBI_TaxID=5741;
                                                                             dehydrogenase gene from the primitive J. Biol. Chem. 267:7539-7544(1992).
                                                                                                                                                                             MEDLINE=92218410;
     SEQUENCE OF 59-261 FROM N.A. MEDLINE=96155200; PubMed=858
                                                                                                                            Yee J., Dennis P.P.; "Isolation and characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Simhes 261;
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       PubMed=8587793;
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                                                                                                     NADP-dependent glutamate
e eucaryote Giardia lamblia.";
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Query Match
Best Local :
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InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog; 1.
PRINTS; PR00082; GLFDHDRGNASE.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M84604; AAA29155.1; -.
EMBL; U47632; AAB05400.1; -.
PIR; A42489; A42489.
HSSP; P24295; 1AUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glutamate dehydrogenase locus.";
Parasitology 112:1-12(1996).
-i- CATALYTIC ACTIVITY: L-glutamate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    + NH(3) + NADPH.
-!- SUBUNIT: Homohexamer (By similarity)
-!- SIMILARITY: Belongs to the Glu/Leu/P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular genetic analysis of Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monis P.T., Mayrhofer G., Andrews R.H.,
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HPKNYQMGANIAGFLKVADSMIEQGCV
                                                                                  AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYN
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                     --VDLAAGANIAGFTKVADAVKAQGAV
                                                                  KGVMYGPAKASNAGGVSVSGLEMSQNSVRLQWTAEEVDQKLRGIMRGIFVACRDTAKKYG
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Pred. No. 4.7e-82;
7; Mismatches 111;
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Complete
SEQUENCE
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MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Westbrock-Wadman S., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

Opportunistic pathogen.";

Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016491; F:oxidoreductase activity; IE
GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog_C.
InterPro; IPR006095; GLFV dehydrog_C.
InterPro; IPR006097; GLFV dehydrog_N.
Pfam; PF00208; GLFV dehydrog; 1.
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Q9HVJ7;
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DLAAGANIAGFTKVADAVKAQGAV
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                                                                 IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSA-MGPSRRYNV
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Last annotation update)
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Pred. No. 5.3e-81;
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GO; GO:0016520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
PF00208; GLFV_dehydrog; 1.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF02811; GLFV_dehydrog; 1.
PRINTS; PR00082; GLFV_dehydrog; N; 1.
PRINTS; PR00082; GLFV_DEHYDROGENASE; 1.
Complete proteome.
SEQUENCE 444 AA; 48490 MW; 8B2CFCCA89EF7DAF
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Q9JY71;
01-OCT-2000
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STRAIN=MC58 / Serogroup B;

MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;

MEDLINE-20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;

Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,

Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,

Dodson R.J., Nelson W.C., Gwinn M.L., Deboy R.T., Peterson J.D.,

Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,

Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,

Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,

Oin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.

Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
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01-OCT-2000 (TrEMBLrel 15, Last sequen
01-JUN-2003 (TrEMBLrel 24, Last annota
Glutamate dehydrogenase, NADP-specific.
OrderedLocusNames=NMB1710;
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TIGR; NMB1710; -.
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VGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK
                                                YAAEKAIQLGAKVLTVSDSNGFVLFPDSGMTEAQLAALIELKEVRRE-RVATYAKEQGLQ
                                                                                                                                                            IRNEFSSYLTGKGLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRYLISGSGNVAQ
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                                                                                  YCAELLLEKGAIVLSLSDSQGYVYEF-NGFTREQLQAVQDMKKKNNSARISEYKSDTAVY
                                                                                                                                                                                                    ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ
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Pred: No. 2e-80;
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Best Local S
Matches 256
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GO; GO:0004354; F:Sulutamate dehydrogenase (NADP+) aci
GO; GO:0016491; F:Sulutamate dehydrogenase (NADP+) aci
GO; GO:0016491; F:Suldoreductase activity; IEA.

InterPro; IPR006520; P:amino acid metabolism; IEA.

InterPro; IPR006095; GLFV dehydrog.

InterPro; IPR006095; GLFV dehydrog_N.

Pfam; PF00208; GLFV dehydrog_N: 1.

Pfam; PF00208; GLFV dehydrog; 1.

Pfam; PF00212; GLFV dehydrog; 1.

PFAm; PF00817; GLFV dehydrog; 1.

PRINTS; PR00082; GLFV dehydrog; 1.
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MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd
Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.,
"Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491.";
Nature Andream M. A. For Access
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SEQUENCE
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01-OCT-2000 (TrEMBLrel. 25, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Glutamate dehydrogenase (EC 1.4.1.4).
Name=gdhA; OrderedLocusNames=NMA1964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
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EMBL; AL162757; CAB85184.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteome; Oxidoreductase.
444 AA; 48462 MW; DE7F1A7B8DD6F424 CRC64;
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                                                                                                                                                                                                                                                                  SWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMG
                                                                                                                                                                                                                                                                                                                                            DINTLEANIKQRNPNQEPEHQAVEEVEMSLDEFLAKNPKYTQQSLLERIVEPERVVMERV
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                                                                                                                  GGKGGSDFDPKGKSDAEVMRFCQAFMTELYRHIGADTDVPAGDIGVGGREIGYLFGQYKK
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                              ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ
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IRNEFSSVLTGKGLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRVLISGSGNVAQ
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nilarity 57.1%;
Conservative 7.
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Pred. No. 5.1e-80;
'2; Mismatches 105
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Query Match
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GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_N.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N, 1.
Pfam; PF02812; GLFV_dehydrog_N, 1.
PFAm; PR00082; GLFV_dehydrog_N, 1.
PFAm; PR00082; GLFV_DEHYDROGENASE; 1.
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Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,

Nelson K.E., Weinel C., Fouts D.E., Gill S.R., Pop M., Holmes M.,

Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,

Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,

Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,

Madupu R., Nelson W.C., White O., Peterson J.D., Tran K.,

Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,

Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,

Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,

Moazzez A., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,

Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002). EMBL; AE016776; AAN66300.1; -. HSSP; P24295; IAUP. TIGR; PP0675; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glutamate dehydrogenase.

Name=gdhA; OrderedLocusNames=PP0675;

Pseudomonas putida (strain KT2440).

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Pseudomonadaceae; Pseudomonas.
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01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
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Q88Q23;
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  WVDDQGKVQVNRGYRIQMSSAIGPYKGGLRFHPSVNLSVLKFLAFEQVFKNSLTSLPMGG
                                                                                            VDNFLARLKORDPGOPEFHOAVEEVLRTLWPFLEANPHYLOSGILERMVEPERAVLFRVS
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Pred. No. 1.6e-79;
5; Mismatches 124;
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GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N,
PF1am; PF00208; GLFV_dehydrog_N;
PF1am; PF00208; GLFV_dehydrog_N;
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01-MAY-1999
01-MAY-1999
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Submitted (JUN-2001) to the I
EMBL; Y12927; CAA73390.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99089647; PubMed-9874251; Wagner J.T., Luedemann H., Faerber P.M., Krauth-Siegel R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=GluDH; Synonyms=GDH;
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-MAY-1999 (TrEMBLrel 21, Last sequence update)
05-JUL-2004 (TrEMBLrel 27, Last annotation update)
Glutamate dehydrogenase (NADP+) (EC 1.4.1.4).
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                                                           48
                                                                                                                                              Similarity
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        MSALKDKTGRFVVLDK-----NASNYESLV----DQEMNNVYERVMKLDPNQVEFLQAF 50
                                                           ISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAV 107
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he EMBL/GenBank/DDBJ
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                                                                                                                   64;
                                                                                                                   Score 1286.5; DB
Pred. No. 1.9e-79;
4; Mismatches 133
                                                                                                                                                                                                                                    50A37C23484C387A CRC64;
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GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog C.
InterPro; IPR006096; GLFV_dehydrog T.
InterPro; IPR006097; GLFV_dehydrog N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF00212; GLFV_dehydrog; 1.
PFAMT; PF00208; GLFV_DEHYDROGENASE; 1.
PROSITE; PR00074; GLFV_DEHYDROGENASE; 1.
SEQUENCE 470 AA; 52546 MM; 50A37C23484C387A CRC
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Q8ILTO;
01-MAR-2003
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MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Garlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subraman G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Frasser C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADP-specific glutamate dehydrogenas ORFNames=PF14_0164; Plasmodium falciparum (isolate 3D7). Eukaryota; Alveolata; Apicomplexa; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                          EMBL; AE014818; AAN36776.1;
HSSP; P24295; 1AUP.
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23, Last sequence update)
25, Last annotation updat
26 dehydrogenase.
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Ansari F.;
Thesis (1994), University of EMBL; Y18494; CAA77192.1; -
EMBL; Y15166; CAA75437.1; -
HSSP; P24295; 1AUP.
GO; GO:0004354; F:glutamate
                                                                                                                                                                                                                                                                                             O9Z3C4 PRELIMINARY; PRT; 445 AA. 09Z3C4; 01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) MADP-glutamate dehydrogenase (EC 1.4.1.4).
                                                                                                              Brown P.R.;
Submitted (OCT-1997)
                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=PAC1;
                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
Pseudomonadaceae; Pseudomo
                                                                           STRAIN=PAO1;
                                                                                                                                     STRAIN-PAC1, and
                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                      Name=gdhA;
                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                          Thesis (1994), University
                                                                                                                                                                                                                                     NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYE
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F:glutamate dehydrogenase
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Pred. No. 1.9e-79
4; Mismatches 13
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   (NADP+) activity;
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Best Local
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GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_N.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N, 1.
Pfam; PF00218; GLFV_dehydrog_N, 1.
Pfam; PF00218; GLFV_dehydrog_N, 1.
PFAM; PR00182; GLFV_DEHYDROGENASE; 1.
PubMed=12820901; DOI=10.1186/1471-2148-3-14;
Andersson J.O., Roger A.J.;
"Evolution of glutamate dehydrogenase genes: everants within and between prokaryotes and euk BMC Evol. Biol. 3:14-14(2003).

EMBL; AF533886; AAPB3853:1; -.

HSSP; P24295; 1AUP.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
                                                                                                                                                                                             Q7YZU7;
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
Glutamate dehydrogenase (
                                                                                                                                                                                                                                                             Q7YZU7
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                   NCBI_TaxID=5722;
                                                                                                                                                 Eukaryota; Parabasalidea; Trichomonada; Trich Trichomonadidae; Trichomonadinae; Trichomonas
                                                                                                                                                                         Trichomonas vaginalis
                                                                                                                                                                                       Name=gdh;
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SEQUENCE 445
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25, Last sec
26, Last and
26, Fragment).
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Pred. No. 2.3e-
56; Mismatches
                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                      Created)
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2.3e-79;
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DT 01-MA
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DE Gluta
GN Name
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OC EUKAR
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RR SEQUE
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Best Local Sim
Matches 255;
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R InterPro; IPR006096; GLFV_dehydrog_C.
R InterPro; IPR006097; GLFV_dehydrog_N.
R Ffam; PF002018; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog; 1.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
NON_TER
1 1
SEQUENCE 437 AA; 47861 MW: 752055547
Yuan P., Stewart T.S.;
Stewart T.S.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ d
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ d
EMBL; AF098675; AAD11789.1; -.

GO: AF098675; IAUP.
GO: GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_N.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
PFAINTS; PR00082; GLFV_dehydrog_N; 1.
                                                                                                                                                                                                                                                                          Q9TXS8;
Q9TXS8;
01-MAY-2000
01-MAY-2000
01-JUN-2003
                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2003 (TrEMBLrel. 24, Glutamate dehydrogenase.
                                                                                                                                                                                                                     Plasmodium falciparum.
Eukaryota; Alveolata;
                                                                                                                                                              STRAIN-FCQ 27;
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  Name=GDH;
                                                                                                                                                                                                       NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.2%; Score 1284.5; DB 59.0%; Pred. No. 2.4e-79; cive 56; Mismatches 118
                                                                                                                                                                                                                    Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                             524
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Best Local Similarity
Matches 258; Conserv
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SEQUENCE 442 AA; 49432 MW; 9D3F8AA679CCE4CC
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                                                                                                                                                                                                                                                                   DPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGV
                                                                                                                                                                                                                                                                                                                       LQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDF
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                                                                                                              WELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCP
                                                                                                                                                                KGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEY--KSDTAVYVGDRRKP
                                                                                                                                                                                                                                                      DPKGKSDNEILKFCQAFMNELYRHIGPCTDVPAGDIGVGGRQIGYLYGQYKKIVNSFNGT
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             AGANIAGFTKVADAVKAQG
                                                                        GKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY---NVDLA
                                                                                                 WGVPC--TLAFPCATQUEINLEDAKLLRKNGCILVGEGANMPSTVDAINLFKSNNIIYCP
                                                                                                                                                    LNVKVLTLSDSNGYVYEPNGFTHENLEFLIDLKEE-KKGRIKEYLNHSSTAKYF-PNEKP
                                                                                                                                                                                                     LTGKNVKWGGSNLRVBATGYGLVYFVLEVLKSLNI PVEKQTAVVSGSGNVALYCVQKLLH
AGANIAGFLKVAESYIEOG
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                                                                                                                                                                                                                                                                                                                                                                                                                   46.5%;
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; Pred. No. 5.3e-78;
57; Mismatches 114;
                       524
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